GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 19, 2002, 03:54:43 ; Search time 272 Seconds
(without alignments)
1275.028 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggccggagctggtcatctc........gagatgaccagctccggccg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	154	100.0	154	24	AAD32908	Plasmid pKS133 2X
c	2	154	100.0	154	24	AAD32908	Plasmid pKS133 2X
c	3	154	100.0	154	24	AAD29231	Plasmids pKS133 2X
c	4	154	100.0	154	24	AAD29231	Plasmids pKS133 2X
c	5	112	72.7	4974	24	ABK10072	Plasmid pKS133 DNA
c	6	112	72.7	4974	24	ABK10072	Plasmid pKS133 DNA
c	7	82.8	53.8	6611	24	AAD32909	pBS68 plasmid used
c	8	82.8	53.8	6611	24	AAD32909	pBS68 plasmid used
c	9	81	52.6	81	24	ABK10711	Artificial DNA seq
c	10	81	52.6	81	24	ABK10711	Artificial DNA seq
c	11	81	52.6	963	24	AAD29247	Plasmid pBS149 2X
c	12	81	52.6	963	24	AAD29247	Plasmid pBS149 2X
c	13	80	51.9	80	24	AAD32907	Plasmids pKS106, p
c	14	80	51.9	80	24	AAD32907	Plasmids pKS106, p
c	15	80	51.9	80	24	AAD29230	Plasmids pKS106, p
c	16	80	51.9	80	24	AAD29230	Plasmids pKS106, p
c	17	80	51.9	92	24	ABK10712	Artificial DNA seq
c	18	80	51.9	92	24	ABK10712	Artificial DNA seq
c	19	80	51.9	92	24	AAD29232	ELVISLIVES complem
c	20	80	51.9	92	24	AAD29232	ELVISLIVES complem
c	21	45.8	29.7	1717	24	AAD29242	Plasmid pBS68 2X E
c	22	45.8	29.7	1717	24	AAD29242	Plasmid pBS68 2X E
c	23	44	28.6	44	24	ABK10710	Artificial DNA seq
c	24	44	28.6	44	24	ABK10710	Artificial DNA seq
c	25	34.8	22.6	1681	24	AAS18438	Contig 115 DNA enc
c	26	34.8	22.6	1681	24	AAS18438	Contig 115 DNA enc
c	27	34.6	22.5	1498	24	AAS59803	Propionibacterium
c	28	34.6	22.5	1498	24	AAS59803	Propionibacterium
c	29	34.6	22.5	6422	23	AAS59655	Propionibacterium
c	30	34.6	22.5	6422	23	AAS59655	Propionibacterium
c	31	34	22.1	4403765	22	AAI99683	Mycobacterium tube
c	32	34	22.1	4411529	22	AAI99682	Mycobacterium tube
c	33	34	22.1	4411529	22	AAI99682	Mycobacterium tube
c	34	33.8	21.9	2821	22	AAI66075	Triticum aestivum
c	35	33.8	21.9	2821	22	AAI66075	Triticum aestivum
c	36	33.2	21.6	1575	22	AAF60762	Psudomonas sp ABC
c	37	33.2	21.6	1575	22	AAF60762	Psudomonas sp ABC
c	38	33	21.4	345	21	AAC04565	Human secreted pro
c	39	33	21.4	345	21	AAC04565	Human secreted pro
c	40	32.8	21.3	9210	22	AAH52046	Mycobacterium tube
c	41	32.8	21.3	9210	22	AAH52046	Mycobacterium tube
c	42	32.8	21.3	4403765	22	AAI99683	Mycobacterium tube
c	43	32.4	21.0	2237	16	AAQ89779	Cotransporter prot
c	44	32.4	21.0	2237	16	AAQ89779	Cotransporter prot
c	45	32	20.8	2119	20	AAX87902	Human cell cycle r

ALIGNMENTS

RESULT 1
AAD32908
ID   AAD32908 standard; DNA; 154 BP.
XX
AC   AAD32908;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
XX
KW   Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW   oil; transgenic plant; gene mapping; immunisation; plasmid pKS133;
KW   gene; ds.
XX
OS   Unidentified.
XX
FH   Key   Location/Qualifiers
FT   CDS   7..36
FT   /*tag= a
FT   /product= "ELVISLIVES protein"
FT   CDS   44..74
FT   /*tag= b
FT   /product= "ELVISLIVES protein"
FT   CDS   complement (82..111)
FT   /*tag= c
FT   /product= "ELVISLIVES protein"
FT   CDS   complement (119..148)
FT   /*tag= d
FT   /product= "ELVISLIVES protein"
XX
PN   WO200216565-A2.
XX

PD   28-FEB-2002.
XX
PF   22-AUG-2001; 2001WO-US26246.
XX
PR   22-AUG-2000; 2000US-226996P.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
DR   WPI; 2002-269353/31.
DR   P-PSDB; AAE20554.
XX
PT   New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT   useful in creating transgenic plants having altered levels of mono-,
PT   poly- and unsaturated fatty acids and in increasing the unsaturation
PT   levels in cellular lipids -
XX
PS   Example 9; Page 43; 77pp; English.
XX
CC   The present invention relates to diverged delta-9 fatty acid desaturase
CC   proteins and polynucleotides encoding such proteins. The nucleic acid
CC   sequences may be used to increase the level of unsaturation in cellular
CC   lipids, including oil, in tissues when the enzyme is absent or rate-
CC   limiting, to isolate cDNAs and genes encoding homologous proteins from
CC   the same or other plant species and to create transgenic plants in which
CC   the polypeptides are present at higher or lower levels than normal or in
CC   cell types or developmental stages in which they are not normally found,
CC   thus altering the level of mono-, poly- and unsaturated fatty acids in
CC   those cells. They are useful as probes for genetic and physical gene
CC   mapping and as markers, e.g. restriction fragment length polymorphism
CC   (RFLP) markers. The peptides can be used to immunise animals to produce
CC   antibodies specific for the peptides and proteins. The present sequence
CC   is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133
CC   This sequence is used in the exemplification of the invention for the
CC   suppression of Fad2 in soybean.
XX
SQ   Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;

Query Match   100.0%; Score 154; DB 24; Length 154;
Best Local Similarity   100.0%; Pred. No. 6.5e-29;
Matches 154;   Conservative   0; Mismatches   0;   Indels   0;   Gaps   0;

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Db   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGACGATCGGCGGCCGGAGCTGGTCATCTCGCT 60

Qy   61 CATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGACGATGAGCGAGATGAGCGAGATGACCAGCTCCGGCGCCG 120
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Db   61 CATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGACGATGAGCGAGATGACCAGCTCCGGCGCCG 120

Qy   121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
           ||||||||||||||||||||||||||||||||||
Db   121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154

RESULT 2
AAD32908/C
ID   AAD32908 standard; DNA; 154 BP.
XX
AC   AAD32908;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.
XX
KW   Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW   oil; transgenic plant; gene mapping; immunisation; plasmid pKS133;
KW   gene; ds.
XX
OS   Unidentified.
XX
FH   Key   Location/Qualifiers

FT   CDS   7..36
FT   /tag=   a
FT   /product=   "ELVISLIVES protein"
FT   CDS   44..74
FT   /tag=   b
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FT   CDS   complement (119..148)
FT   /tag=   d
FT   /product=   "ELVISLIVES protein"
XX
PN   WO200216565-A2.
XX
PD   28-FEB-2002.
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PF   22-AUG-2001; 2001WO-US26246.
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PR   22-AUG-2000; 2000US-226996P.
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PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
DR   WPI; 2002-269353/31.
DR   P-PSDB; AAE20554.
XX
PT   New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT   useful in creating transgenic plants having altered levels of mono-,
PT   poly- and unsaturated fatty acids and in increasing the unsaturation
PT   levels in cellular lipids -
XX
PS   Example 9; Page 43; 77pp; English.
XX
CC   The present invention relates to diverged delta-9 fatty acid desaturase
CC   proteins and polynucleotides encoding such proteins. The nucleic acid
CC   sequences may be used to increase the level of unsaturation in cellular
CC   lipids, including oil, in tissues when the enzyme is absent or rate-
CC   limiting, to isolate cDNAs and genes encoding homologous proteins from
CC   the same or other plant species and to create transgenic plants in which
CC   the polypeptides are present at higher or lower levels than normal or in
CC   cell types or developmental stages in which they are not normally found,
CC   thus altering the level of mono-, poly- and unsaturated fatty acids in
CC   those cells. They are useful as probes for genetic and physical gene
CC   mapping and as markers, e.g. restriction fragment length polymorphism
CC   (RFLP) markers. The peptides can be used to immunise animals to produce
CC   antibodies specific for the peptides and proteins. The present sequence
CC   is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133
CC   This sequence is used in the exemplification of the invention for the
CC   suppression of Fad2 in soybean.
XX
SQ   Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;

Query Match   100.0%; Score 154; DB 24; Length 154;
Best Local Similarity   100.0%; Pred. No. 6.5e-29;
Matches 154;   Conservative   0; Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGACGATCGGCGGCCGGAGCTGGTCATCTCGCT 60
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Qy   61 CATCGTCGAGTCGGCGGCCGGACTCGACGATCGCGCGGCCGGAGCTGGTCATCTCGCT 120
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Qy   121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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Qy   121 ACTCGACGATGAGCGAGATGACCACCAGCTCCGCCG 154
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Db   121 ACTCGACGATGAGCGAGATGACCAGCTCCGCCG 154
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RESULT 4
AAD29231/c

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AC   AAD29231;
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DT   07-MAY-2002 (first entry)
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DE   Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
XX
KW   Recombinant construct; gene expression; plasmid pKS133; ds.
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OS   Unidentified.
XX
XX
FH   Key             Location/Qualifiers
FT   CDS             7..36
FT                   /tag= a
FT                   /product= "ELVISLIVES protein"
FT   CDS             44..74
FT                   /tag= b
FT                   /product= "ELVISLIVES protein"
FT   CDS             complement (82..111)
FT                   /tag= c
FT                   /product= "ELVISLIVES protein"
FT   CDS             complement (119..148)
FT                   /tag= d
FT                   /product= "ELVISLIVES protein"
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PN   WO20020090904-A2.
XX
PD   03-JAN-2002.
XX
PF   22-JUN-2001; 2001WO-US19962.
XX
PR   23-JUN-2000; 2000US-213961P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI   Nichols SE;
XX
DR   WPI; 2002-139927/18.
DR   P-PSDB; AAE18333.
XX
PT   New recombinant construct having a promoter operably linked to a DNA
PT   sequence which when expressed produces an RNA having homology to a
PT   target mRNA and its reverse complement unrelated to endogenous DNA, for
PT   reducing gene expression -
XX
PS   Claim 45; Page 37; 77pp; English.
XX
CC   The present invention relates to a new recombinant construct. The
CC   construct comprises a promoter operably linked to a DNA sequence which
CC   when expressed by a host produces an RNA having homology to at least one
CC   target mRNA expressed by the host and complementary RNA regions. The
CC   recombinant construct is useful for reducing the expression of a target
CC   mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC   recombinant constructs are also used in reducing expression of a target
CC   mRNA or any similar endogenous mRNA. The sequences and their reverse
CC   complements can be used to reduce the expression of any endogenous
CC   genomic sequence that shares substantial similarity to nucleic acid
CC   fragment which is in proximity to the DNA or RNA sequence derived from
CC   it. The present sequence is 2X ELVISLIVES complementary repeat region
CC   DNA found in plasmid pKS133 used in the exemplification of the invention.
XX
SQ   Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;
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Query Match          100.0%;   Score 154;   DB 24;   Length 154;
Best Local Similarity 100.0%;  Pred. No. 6.5e-29;
Matches  154;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTGGTCATCTCGCT 60
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```
CC   it. The present sequence is 2X ELVISLIVES complementary repeat region
CC   DNA found in plasmid pKS133 used in the exemplification of the invention.
XX
SQ   Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 other;

Query Match             100.0%;  Score 154;  DB 24;  Length 154;
Best Local Similarity   100.0%;  Pred. No. 6.5e-29;
Matches  154;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60
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Qy   61 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGACGAGCTCCGGCCG 120
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Db   94 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGACGAGCTCCGGCCG 35

Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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Db   34 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 1


RESULT 5
ABK10072
ID   ABK10072 standard; DNA; 4974 BP.
XX
AC   ABK10072;
XX
DT   05-JUN-2002 (first entry)
XX
DE   Plasmid pKS133 DNA.
XX
KW   Plastidic phosphoglucomutase; gene; ds; plasmid pKS133.
XX
OS   Synthetic.
XX
PN   EP1174510-A2.
XX
PD   23-JAN-2002.
XX
PF   17-JUL-2001; 2001EP-0306143.
XX
PR   17-JUL-2000; 2000US-218712P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR   WPI; 2002-156692/21.
XX
PT   Novel isolated polypeptides having phosphoglucomutase activity and
PT   polynucleotides encoding the polypeptides, useful for producing
PT   transgenic plants with altered plastidic phosphoglucomutase protein
PT   levels -
XX
PS   Example 9; SEQ ID No 17; 27pp; English.
XX
CC   The invention relates to plastidic phosphoglucomutase polypeptides and
CC   their related nucleic acids. The sequences are useful for producing a
CC   transgenic plant, by transforming a plant cell with a polynucleotide of
CC   the invention and regenerating a plant from the transformed plant cell.
CC   Polynucleotide fragments are useful for suppressing the level of
CC   expression of a gene encoding a polypeptide having plastidic
CC   phosphoglucomutase activity. An isolated polynucleotide that affects the
CC   level of expression of a plastidic phosphoglucomutase polypeptide in a
CC   plant cell can be identified by introducing a DNA fragment comprising at
CC   least 541 nucleotides, measuring the level of the polypeptide in the
CC   plant cell containing the polynucleotide, and comparing the level of the
CC   polypeptide in the plant cell containing the isolated polynucleotide with
CC   the level of the polypeptide in a plant cell that does not contain the
CC   isolated polynucleotide. A method for altering the level of expression of
CC   a plastidic phosphoglucomutase protein in a host cell comprises
CC   transforming a host cell with a chimeric gene and growing the transformed
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CC   cell under conditions that are suitable for expression of the chimeric
CC   gene, where the expression of the gene results in production of altered
CC   levels of plastidic phosphoglucomutase. This sequence represents plasmid
CC   DNA used in the methods of the invention.
CC   Note: This sequence is not represented in the printed specification but
CC   is based on sequence information supplied by the European Patent Office.
XX
SQ   Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 1 other;

Query Match             72.7%;  Score 112;  DB 24;  Length 4974;
Best Local Similarity  100.0%;  Pred. No. 1.3e-1B;
Matches  112;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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RESULT 6
ABK10072/c
ID   ABK10072 standard; DNA; 4974 BP.
XX
AC   ABK10072;
XX
DT   05-JUN-2002 (first entry)
XX
DE   Plasmid pKS133 DNA.
XX
KW   Plastidic phosphoglucomutase; gene; ds; plasmid pKS133.
XX
OS   Synthetic.
XX
PN   EP1174510-A2.
XX
PD   23-JAN-2002.
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PF   17-JUL-2001; 2001EP-0306143.
XX
PR   17-JUL-2000; 2000US-218712P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR   WPI; 2002-156692/21.
XX
PT   Novel isolated polypeptides having phosphoglucomutase activity and
PT   polynucleotides encoding the polypeptides, useful for producing
PT   transgenic plants with altered plastidic phosphoglucomutase protein
PT   levels -
XX
PS   Example 9; SEQ ID No 17; 27pp; English.
XX
CC   The invention relates to plastidic phosphoglucomutase polypeptides and
CC   their related nucleic acids. The sequences are useful for producing a
CC   transgenic plant, by transforming a plant cell with a polynucleotide of
CC   the invention and regenerating a plant from the transformed plant cell.
CC   Polynucleotide fragments are useful for suppressing the level of
CC   expression of a gene encoding a polypeptide having plastidic
CC   phosphoglucomutase activity. An isolated polynucleotide that affects the
CC   level of expression of a plastidic phosphoglucomutase polypeptide in a
CC   plant cell can be identified by introducing a DNA fragment comprising at
CC   least 541 nucleotides, measuring the level of the polypeptide in the
CC   plant cell containing the polynucleotide, and comparing the level of the
CC   polypeptide in the plant cell containing the isolated polynucleotide with
CC   the level of the polypeptide in a plant cell that does not contain the
CC   isolated polynucleotide. A method for altering the level of expression of
CC   a plastidic phosphoglucomutase protein in a host cell comprises
CC   transforming a host cell with a chimeric gene and growing the transformed
```

CC   cell under conditions that are suitable for expression of the chimeric
CC   gene, where the expression of the gene results in production of altered
CC   levels of plastidic phosphoglucomutase. This sequence represents plasmid
CC   DNA used in the methods of the invention.
CC   Note: This sequence is not represented in the printed specification but
CC   is based on sequence information supplied by the European Patent Office.
XX
SQ   Sequence 4974 BP: 1444 A; 1070 C; 1003 G; 1456 T; 1 other;

Query Match   72.7%;   Score 112;   DB 24;   Length 4974;
Best Local Similarity 100.0%;   Pred. No. 1.3e-18;
Matches 112;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCCGCCGACTCGACGATGAGCCGAGAT 102
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Qy 103 GACCAGCTCCGGCCGCCGACTCGACGATGATGAGCCGAGATGACCAGCTCCGGCCG 154
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4914 GACCAGCTCCGGCCGCCGACTCGACGATGAGCCGAGATGACCAGCTCCGGCCG 4863

RESULT 7
AAD32909
ID   AAD32909 standard; DNA; 6611 BP.
XX
AC   AAD32909;
XX
DT   01-JUL-2002 (first entry)
XX
DE   pBS68 plasmid used for diverged delta-9 desaturase suppression.
XX
KW   Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW   oil; transgenic plant; gene mapping; immunisation; plasmid pBS68; ds.
XX
OS   Unidentified.
XX
FH   Key   Location/Qualifiers
FT   terminator   523..725
FT   /*tag= b
FT   /label= Kit3_terminator
FT   misc_feature   complement (880..1920)
FT   /*tag= b
FT   /note= "Hygromycin selection region"
FT   promoter   3260..5348
FT   /*tag= c
FT   /label= Kit3_promoter
XX
PN   WO200216565-A2.
XX
PD   28-FEB-2002.
XX
PF   22-AUG-2001; 2001WO-US26246.
XX
PR   22-AUG-2000; 2000US-226996P.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
DR   WPI; 2002-269353/31.
XX
PT   New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT   useful in creating transgenic plants having altered levels of mono-,
PT   poly- and unsaturated fatty acids and in increasing the unsaturation
PT   levels in cellular lipids -
XX
PS   Example 9; Page 76-77; 77pp; English.
XX
CC   The present invention relates to diverged delta-9 fatty acid desaturase
CC   proteins and polynucleotides encoding such proteins. The nucleic acid
CC   sequences may be used to increase the level of unsaturation in cellular
CC   lipids, including oil, in tissues when the enzyme is absent or rate-

CC   limiting, to isolate cDNAs and genes encoding homologous proteins from
CC   the same or other plant species and to create transgenic plants in which
CC   the polypeptides are present at higher or lower levels than normal or in
CC   cell types or developmental stages in which they are not normally found,
CC   thus altering the level of mono-, poly- and unsaturated fatty acids in
CC   those cells. They are useful as probes for genetic and physical gene
CC   mapping and as markers, e.g. restriction fragment length polymorphism
CC   (RFLP) markers. The peptides can be used to immunise animals to produce
CC   antibodies specific for the peptides and proteins. The present sequence
CC   is plasmid pBS68 which is used for the suppression of diverged delta-9
CC   desaturase in high stearate phenotypes. This sequence is used in the
CC   exemplification of the invention.
CC   Note: The sequence data for this sequence (AAD32909) corresponding to
CC   position 1501 to 6611 is not represented in the printed specification
CC   but is based on the sequence information supplied by the European patent
CC   office.
XX
SQ   Sequence 6611 BP: 1831 A; 1472 C; 1453 G; 1854 T; 1 other;

Query Match   53.8%;   Score 82.8;   DB 24;   Length 6611;
Best Local Similarity 97.7%;   Pred. No. 1.7e-11;
Matches 84;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCCGCCGAGCTGGTCATCTCGCT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5348 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCCGCCGAGCTGGTCATCTCGCT 5407

Qy   61 CATCGTCGAGTCGGCCGGCCGCCGACT 86
         ||||||||||||||||||||| ||
Db 5408 CATCGTCGAGTCGGCCGGCCGCCGCTGAGT 5433

RESULT 8
AAD32909/c
ID   AAD32909 standard; DNA; 6611 BP.
XX
AC   AAD32909;
XX
DT   01-JUL-2002 (first entry)
XX
DE   pBS68 plasmid used for diverged delta-9 fatty acid desaturase suppression.
XX
KW   Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW   oil; transgenic plant; gene mapping; immunisation; plasmid pBS68; ds.
XX
OS   Unidentified.
XX
FH   Key   Location/Qualifiers
FT   terminator   523..725
FT   /*tag= b
FT   /label= Kit3_terminator
FT   misc_feature   complement (880..1920)
FT   /*tag= b
FT   /note= "Hygromycin selection region"
FT   promoter   3260..5348
FT   /*tag= c
FT   /label= Kit3_promoter
XX
PN   WO200216565-A2.
XX
PD   28-FEB-2002.
XX
PF   22-AUG-2001; 2001WO-US26246.
XX
PR   22-AUG-2000; 2000US-226996P.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
DR   WPI; 2002-269353/31.
XX
PT   New delta-9 fatty acid desaturase polypeptides and polynucleotides,

```
PT   useful in creating transgenic plants having altered levels of mono-,
PT   poly- and unsaturated fatty acids and in increasing the unsaturation
PT   levels in cellular lipids -
XX
PS   Example 9; Page 76-77; 77pp; English.
XX
CC   The present invention relates to diverged delta-9 fatty acid desaturase
CC   proteins and polynucleotides encoding such proteins. The nucleic acid
CC   sequences may be used to increase the level of unsaturation in cellular
CC   lipids, including oil, in tissues when the enzyme is absent or rate-
CC   limiting, to isolate cDNAs and genes encoding homologous proteins from
CC   the same or other plant species and to create transgenic plants in which
CC   the polypeptides are present at higher or lower levels than normal or in
CC   cell types or developmental stages in which they are not normally found,
CC   thus altering the level of mono-, poly- and unsaturated fatty acids in
CC   those cells. They are useful as probes for genetic and physical gene
CC   mapping and as markers, e.g. restriction fragment length polymorphism
CC   (RFLP) markers. The peptides can be used to immunise animals to produce
CC   antibodies specific for the peptides and proteins. The present sequence
CC   is plasmid pBS68 which is used for the suppression of diverged delta-9
CC   desaturase in high stearate phenotypes. This sequence is used in the
CC   exemplification of the invention.
CC   Note: The sequence data for this sequence (AAD32909) corresponding to
CC   position 1501 to 6611 is not represented in the printed specification
CC   but is based on the sequence information supplied by the European patent
CC   office.
XX
SQ   Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 1 other;

Query Match             53.8%;   Score 82.8;  DB 24;  Length 6611;
Best Local Similarity   97.7%;          Pred. No. 1.7e-11;
Matches   84;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy     69 AGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 128
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5433 ACTCAGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 5374

Qy    129 ATGAGCGAGATGACCAGCTCCGGCCG 154
          ||||||||||||||||||||||||||
Db   5373 ATGAGCGAGATGACCAGCTCCGGCCG 5348


RESULT 9
ABK10711
ID   ABK10711 standard; DNA; 81 BP.
XX
AC   ABK10711;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Artificial DNA sequence #3.
XX
KW   Plastidic phosphoglucomutase; transgenic; plant; gene; ds.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   CDS            7..36
FT                  /tag= a
FT                  /product= "ELVISLIVES peptide"
FT                  /partial
FT                  /note= "No start or stop codon shown"
FT   CDS            44..73
FT                  /tag= b
FT                  /product= "ELVISLIVES peptide"
FT                  /partial
FT                  /note= "No start or stop codon shown"
XX
PN   EP1174510-A2.
XX
PD   23-JAN-2002.
XX
PF   17-JUL-2001; 2001EP-0306143.
```

```
XX
PR   17-JUL-2000; 2000US-218712P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR   WPI; 2002-156692/21.
DR   P-PSDB; AAU7109.
XX
PT   Novel isolated polypeptides having phosphoglucomutase activity and
PT   polynucleotides encoding the polypeptides, useful for producing
PT   transgenic plants with altered plastidic phosphoglucomutase protein
PT   levels -
XX
PS   Example 9; Page 19; 27pp; English.
XX
CC   The invention relates to plastidic phosphoglucomutase polypeptides and
CC   their related nucleic acids. The sequences are useful for producing a
CC   transgenic plant, by transforming a plant cell with a polynucleotide of
CC   the invention and regenerating a plant from the transformed plant cell.
CC   Polynucleotide fragments are useful for suppressing the level of
CC   expression of a gene encoding a polypeptide having plastidic
CC   phosphoglucomutase activity. An isolated polynucleotide that affects the
CC   level of expression of a plastidic phosphoglucomutase polypeptide in a
CC   plant cell can be identified by introducing a DNA fragment comprising at
CC   least 541 nucleotides, measuring the level of the polypeptide in the
CC   plant cell containing the polynucleotide, and comparing the level of the
CC   polypeptide in the plant cell containing the isolated polynucleotide with
CC   the level of the polypeptide in a plant cell that does not contain the
CC   isolated polynucleotide. A method for altering the level of expression of
CC   a plastidic phosphoglucomutase protein in a host cell comprises
CC   transforming a host cell with a chimeric gene and growing the transformed
CC   cell under conditions that are suitable for expression of the chimeric
CC   gene, where the expression of the gene results in production of altered
CC   levels of plastidic phosphoglucomutase. This sequence represents an
CC   artificial DNA used for plasmid construction, in the methods of the
CC   invention.
XX
SQ   Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 other;

Query Match             52.6%;   Score 81;  DB 24;  Length 81;
Best Local Similarity   100.0%;          Pred. No. 3.8e-11;
Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CGGCCGGAGCGTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CGGCCGGAGCGTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60

Qy     61 CATCGTCGAGTCGGCGGCCGC 81
          |||||||||||||||||||||
Db     61 CATCGTCGAGTCGGCGGCCGC 81


RESULT 10
ABK10711/c
ID   ABK10711 standard; DNA; 81 BP.
XX
AC   ABK10711;
XX
DT   05-JUN-2002  (first entry)
XX
DE   Artificial DNA sequence #3.
XX
KW   Plastidic phosphoglucomutase; transgenic; plant; gene; ds.
XX
OS   Synthetic.
XX
FH   Key            Location/Qualifiers
FT   CDS            7..36
FT                  /tag= a
FT                  /product= "ELVISLIVES peptide"
FT                  /partial
```

FT   CDS   /note= "No start or stop codon shown"
FT   44..73
FT   /*tag= b
FT   /product= "ELVISLIVES peptide"
FT   /partial
FT   /note= "No start or stop codon shown"
XX
PN   EP1174510-A2.
XX
PD   23-JAN-2002.
XX
PF   17-JUL-2001; 2001EP-0306143.
XX
PR   17-JUL-2000; 2000US-218712P.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI   Allen SM, Butler KH, Carlson TJ, Ilag LL;
XX
DR   WPI; 2002-156692/21.
DR   P-PSDB; AAD77109.
XX
PT   Novel isolated polypeptides having phosphoglucomutase activity and
PT   polynucleotides encoding the polypeptides, useful for producing
PT   transgenic plants with altered plastidic phosphoglucomutase protein
PT   levels -
XX
PS   Example 9; Page 19; 27pp; English.
XX
CC   The invention relates to plastidic phosphoglucomutase polypeptides and
CC   their related nucleic acids. The sequences are useful for producing a
CC   transgenic plant, by transforming a plant cell with a polynucleotide of
CC   the invention and regenerating a plant from the transformed plant cell.
CC   Polynucleotide fragments are useful for suppressing the level of
CC   expression of a gene encoding a polypeptide having plastidic
CC   phosphoglucomutase activity. An isolated polynucleotide that affects the
CC   level of expression of a plastidic phosphoglucomutase polypeptide in a
CC   plant cell can be identified by introducing a DNA fragment comprising at
CC   least 541 nucleotides, measuring the level of the polypeptide in the
CC   plant cell containing the polynucleotide, and comparing the level of the
CC   polypeptide in the plant cell containing the isolated polynucleotide with
CC   the level of the polypeptide in a plant cell that does not contain the
CC   isolated polynucleotide. A method for altering the level of expression of
CC   a plastidic phosphoglucomutase protein in a host cell comprises
CC   transforming a host cell with a chimeric gene and growing the transformed
CC   cell under conditions that are suitable for expression of the chimeric
CC   gene, where the expression of the gene results in production of altered
CC   levels of plastidic phosphoglucomutase. This sequence represents an
CC   artificial DNA used for plasmid construction, in the methods of the
CC   invention.
XX
SQ   Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 other;

Query Match   52.6%; Score 81; DB 24; Length 81;
Best Local Similarity   100.0%; Pred. No. 3.8e-11;
Matches   81; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   74 GCGGCGCCGCCACTCGACGATGAGCGAGGAGATGACCAGCTCCGGCCGGCCGACTCGACGATGAG 133
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   81 GCGGCGCCGCCACTCGACGATGAGCGAGGAGATGACCAGCTCCGGCCGGCCGACTCGACGATGAG 133

Qy   134 CGAGATGACCAGCTCCGGCCG 154
               |||||||||||||||||||||
Db   21 CGAGATGACCAGCTCCGGCCG 1

RESULT 11
AAD29247
ID   AAD29247 standard; DNA; 963 BP.
XX
AC   AAD29247;
XX
DT   07-MAY-2002 (first entry)

XX
DE   Plasmid pBS149 2X ELVISLIVES complementary region DNA.
XX
KW   Recombinant construct; gene expression; late-soybean-embryo promoter;
KW   LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
XX
OS   Unidentified.
XX
PN   WO200200904-A2.
XX
PD   03-JAN-2002.
XX
PF   22-JUN-2001; 2001WO-US19962.
XX
PR   23-JUN-2000; 2000US-213961P.
XX
PA   (DUPO) DU PONT DE NEMOURS & CO E I.
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI   Nichols SE;
XX
DR   WPI; 2002-139927/18.
XX
PT   New recombinant construct having a promoter operably linked to a DNA
PT   sequence which when expressed produces an RNA having homology to a
PT   target mRNA and its reverse complement unrelated to endogenous DNA, for
PT   reducing gene expression -
XX
PS   Example 10; Page 72; 77pp; English.
XX
CC   The present invention relates to a new recombinant construct. The
CC   construct comprises a promoter operably linked to a DNA sequence which
CC   when expressed by a host produces an RNA having homology to at least one
CC   target mRNA expressed by the host and complementary RNA regions. The
CC   recombinant construct is useful for reducing the expression of a target
CC   mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC   recombinant constructs are also used in reducing expression of a target
CC   mRNA or any similar endogenous mRNA. The sequences and their reverse
CC   complements can be used to reduce the expression of any endogenous
CC   genomic sequence that shares substantial similarity to nucleic acid
CC   fragment which is in proximity to the DNA or RNA sequence derived from
CC   it. The present sequence is 2X ELVISLIVES complementary region from
CC   pBS149 that contains fragments from two soybean galactinol synthase genes
CC   GAS1 and GAS2. The region is functionally attached to a late-soybean-
CC   embryo promoter (LEA) and a phaseolin 3' terminator region. This
CC   entire region is then cloned into BamHI site of pKS136, which contains a
CC   2X ELVISLIVES complementary region controlled by a soybean Kti promoter
CC   and terminator region used in the exemplification of the invention.
XX
SQ   Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 other;

Query Match   52.6%; Score 81; DB 24; Length 963;
Best Local Similarity   100.0%; Pred. No. 4.3e-11;
Matches   81; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   74 GCGGCGCCGCCACTCGACGATGAGCGAGGAGATGACCAGCTCCGGCCGGCCGACTCGACGATGAG 133
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   883 GCGGCGCCGCCACTCGACGATGAGCGAGGAGATGACCAGCTCCGGCCGGCCGACTCGACGATGAG 942

Qy   134 CGAGATGACCAGCTCCGGCCG 154
               |||||||||||||||||||||
Db   943 CGAGATGACCAGCTCCGGCCG 963

RESULT 12
AAD29247/c
ID   AAD29247 standard; DNA; 963 BP.
XX
AC   AAD29247;
XX
DT   07-MAY-2002 (first entry)
XX

```
DE    Plasmid pBS149 2X ELVISLIVES complementary region DNA.
XX
KW    Recombinant construct; gene expression; late-soybean-embryo promoter;
KW    LEA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
XX
OS    Unidentified.
XX
PN    WO200200904-A2.
XX
PD    03-JAN-2002.
XX
PF    22-JUN-2001; 2001WO-US19962.
XX
PR    23-JUN-2000; 2000US-213961P.
XX
PA    (DUPO ) DU PONT DE NEMOURS & CO E I.
PA    (PION-) PIONEER HI-BRED INT INC.
XX
PI    Glassman KF,  Gordon-Kamm WJ,  Kinney AJ,  Lowe K,  Stecca KL;
PI    Nichols SE;
XX
DR    WPI; 2002-139927/18.
XX
PT    New recombinant construct having a promoter operably linked to a DNA
PT    sequence which when expressed produces an RNA having homology to a
PT    target mRNA and its reverse complement unrelated to endogenous DNA, for
PT    reducing gene expression -
XX
PS    Example 10; Page 72; 77pp; English.
XX
CC    The present invention relates to a new recombinant construct. The
CC    construct comprises a promoter operably linked to a DNA sequence which
CC    when expressed by a host produces an RNA having homology to at least one
CC    genomic sequence that shares substantial similarity to nucleic acid
CC    fragment which is in proximity to the DNA or RNA sequence derived from
CC    it. The present sequence is 2X ELVISLIVES complementary region from
CC    pBS149 that contains fragments from two soybean galactinol synthase genes
CC    GAS1 and GAS2. The region is functionally attached to a late-soybean-
CC    embryo promoter (LEA) and a phaseolin 3' terminator region. This
CC    entire region is then cloned into BamHI site of pKS136, which contains a
CC    2X ELVISLIVES complementary region controlled by a soybean Kti promoter
CC    and terminator region used in the exemplification of the invention.
XX
SQ    Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 other;

Query Match     52.6%;  Score 81;  DB 24;  Length 963;
Best Local Similarity   100.0%;  Pred. No. 4.3e-11;
Matches   81;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTCGGTCATCTCGCT 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    963 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTCGGTCATCTCGCT 904

Qy     61 CATCGTCGAGTCGGCGGCCGC 81
          |||||||||||||||||||||
Db    903 CATCGTCGAGTCGGCGGCCGC 883

RESULT 13
AAD32907
ID    AAD32907 standard; DNA; 80 BP.
XX
AC    AAD32907;
XX
DT    01-JUL-2002 (first entry)
XX
DE    Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
```

```
DE    Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
XX
KW    oil; transgenic plant; gene mapping; immunisation; plasmid pKS124;
KW    plasmid pKS106; gene; ds.
XX
OS    Unidentified.
XX
FH    Key         Location/Qualifiers
FT    CDS         7..36
FT                /tag= a
FT                /product= "ELVISLIVES protein"
FT    CDS         complement (45..74)
FT                /tag= b
FT                /product= "ELVISLIVES protein"
XX
PN    WO200216565-A2.
XX
PD    28-FEB-2002.
XX
PF    22-AUG-2001; 2001WO-US26246.
XX
PR    22-AUG-2000; 2000US-226996P.
XX
PA    (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI    Booth JR,  Cahoon RE,  Hitz WD,  Kinney AJ,  Yadav NS;
XX
DR    WPI; 2002-269353/31.
DR    P-PSDB; AAE20554.
XX
PT    New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT    useful in creating transgenic plants having altered levels of mono-,
PT    poly- and unsaturated fatty acids and in increasing the unsaturation
PT    levels in cellular lipids -
XX
PS    Example 9; Page 43; 77pp; English.
XX
CC    The present invention relates to diverged delta-9 fatty acid desaturase
CC    proteins and polynucleotides encoding such proteins. The nucleic acid
CC    sequences may be used to increase the level of unsaturation in cellular
CC    lipids, including oil, in tissues when the enzyme is absent or rate-
CC    limiting, to isolate cDNAs and genes encoding homologous proteins from
CC    the same or other plant species and to create transgenic plants in which
CC    the polypeptides are present at higher or lower levels than normal or in
CC    cell types or developmental stages in which they are not normally found,
CC    thus altering the level of mono-, poly- and unsaturated fatty acids in
CC    those cells. They are useful as probes for genetic and physical gene
CC    mapping and as markers, e.g. restriction fragment length polymorphism
CC    (RFLP) markers. The peptides can be used to immunise animals to produce
CC    antibodies specific for the peptides and proteins. The present sequence
CC    is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106
CC    and pKS124. This sequence is used in the exemplification of the invention
CC    for the suppression of Fad2 in soybean.
XX
SQ    Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 other;

Query Match     51.9%;  Score 80;  DB 24;  Length 80;
Best Local Similarity   100.0%;  Pred. No. 6.7e-11;
Matches   80;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTCGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGTCGACGATGAGC 97
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGCTCGGTCATCTCGCTCATCGTCGAGTCGGCGCCGGAGTCGACGATGAGC 60

Qy     98 GAGATGACCAGCTCCGGCCG 117
          ||||||||||||||||||||
Db     61 GAGATGACCAGCTCCGGCCG 80

RESULT 14
AAD32907/c
ID    AAD32907/c standard; DNA; 80 BP.
XX
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Left column

```
AC
XX
DT   AAD32907;
XX
DT   01-JUL-2002 (first entry)
XX
DE   Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
KW   Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
KW   oil; transgenic plant; gene mapping; immunisation; plasmid pKS124;
KW   plasmid pKS106; gene; ds.
XX
OS   Unidentified.
XX
FH   Key            Location/Qualifiers
FH
FT   CDS            7..36
FT                  /tag= a
FT                  /product= "ELVISLIVES protein"
FT   CDS            complement (45..74)
FT                  /tag= b
FT                  /product= "ELVISLIVES protein"
XX
PN   WO200215565-A2.
XX
PD   28-FEB-2002.
XX
PF   22-AUG-2001; 2001WO-US26246.
XX
PR   22-AUG-2000; 2000US-226996P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
DR   WPI; 2002-269353/31.
DR   P-PSDB; AAE20554.
XX
PT   New delta-9 fatty acid desaturase polypeptides and polynucleotides,
PT   useful in creating transgenic plants having altered levels of mono-,
PT   poly- and unsaturated fatty acids and in increasing the unsaturation
PT   levels in cellular lipids -
XX
PS   Example 9; Page 43; 77pp; English.
XX
CC   The present invention relates to diverged delta-9 fatty acid desaturase
CC   proteins and polynucleotides encoding such proteins. The nucleic acid
CC   sequences may be used to increase the level of unsaturation in cellular
CC   lipids, including oil, in tissues when the enzyme is absent or rate-
CC   limiting, to isolate cDNAs and genes encoding homologous proteins from
CC   the same or other plant species and to create transgenic plants in which
CC   the polypeptides are present at higher or lower levels than normal or in
CC   cell types or developmental stages in which they are not normally found,
CC   thus altering the level of mono-, poly- and unsaturated fatty acids in
CC   those cells. They are useful as probes for genetic and physical gene
CC   mapping and as markers, e.g. restriction fragment length polymorphism
CC   (RFLP) markers. The peptides can be used to immunise animals to produce
CC   antibodies specific for the peptides and proteins. The present sequence
CC   is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106
CC   and pKS124. This 1X ELVISLIVES complementary repeat region of the invention
CC   for the suppression of Fad2 in soybean.
XX
SQ   Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 other;

Query Match    51.9%;  Score 80;  DB 24;  Length 80;
Best Local Similarity  100.0%;  Pred. No. 6.7e-11;
Matches  80;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 97
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 21

Qy   98 GAGATGACCAGCTCCGGCCG 117
        |||||||||||||
Db   20 GAGATGACCAGCTCCGGCCG 1
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Right column

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RESULT 15
AAD29230
ID   AAD29230 standard; DNA; 80 BP.
XX
AC   AAD29230;
XX
DT   07-MAY-2002 (first entry)
XX
DE   Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
KW   Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
KW   ds.
XX
OS   Unidentified.
XX
FH   Key            Location/Qualifiers
FH
FT   CDS            7..36
FT                  /tag- a
FT                  /product= "ELVISLIVES protein"
FT   CDS            complement (45..74)
FT                  /tag- b
FT                  /product= "ELVISLIVES protein"
XX
PN   WO200200904-A2.
XX
PD   03-JAN-2002.
XX
PF   22-JUN-2001; 2001WO-US19962.
XX
PR   23-JUN-2000; 2000US-213961P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
PI   Nichols SE;
XX
DR   WPI; 2002-139927/18.
DR   P-PSDB; AAE18333.
XX
PT   New recombinant construct having a promoter operably linked to a DNA
PT   sequence which when expressed produces an RNA having homology to a
PT   target mRNA and its reverse complement unrelated to endogenous DNA, for
PT   reducing gene expression -
XX
PS   Claim 45; Page 37; 77pp; English.
XX
CC   The present invention relates to a new recombinant construct. The
CC   construct comprises a promoter operably linked to a DNA sequence which
CC   when expressed by a host produces an RNA having homology to at least one
CC   target mRNA expressed by the host and complementary RNA regions. The
CC   recombinant construct is useful for reducing the expression of a target
CC   mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC   recombinant constructs are also used in reducing expression of a target
CC   mRNA or any similar endogenous mRNA. The sequences and their reverse
CC   complements can be used to reduce the expression of any endogenous
CC   genomic sequence that shares substantial similarity to nucleic acid
CC   fragment which is in proximity to the DNA or RNA sequence derived from
CC   it. The present sequence is 1X ELVISLIVES complementary repeat region
CC   DNA found in plasmids pKS106 and pKS124 used in the exemplification of
CC   the invention.
XX
SQ   Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 other;

Query Match    51.9%;  Score 80;  DB 24;  Length 80;
Best Local Similarity  100.0%;  Pred. No. 6.7e-11;
Matches  80;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 97
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 60
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us-09-887-194a-13.rng

Tue Nov 19 10:31:21 2002

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Qy    98 GAGATGACCAGCTCCGGCCG 117
         |||||||||||||||||||
Db    61 GAGATGACCAGCTCCGGCCG 80

Search completed: November 19, 2002, 05:24:32
Job time : 302 secs
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                    GenCore version 5.1.3
              Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        November 19, 2002, 04:09:45 ; Search time 54 Seconds
                                 (without alignments)
                          874.597 Million cell updates/sec

Title:          US-09-887-194A-13
Perfect score:  154
Sequence:       1 cggccggagctggtcatctc.........gagatgaccagctccggccg 154

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:       882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Issued_Patents_NA:*
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        2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
        3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
        4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
        5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
        6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		34.8	22.6	1681	4	US-09-434-288-7	Sequence 7, Appli
2		34.8	22.6	1681	4	US-09-43-288-7	Sequence 7, Appli
3	c	34	22.1	4403765	4	US-09-103-840A-2	Sequence 2, Appli
4	c	34	22.1	4411529	4	US-09-103-840A-1	Sequence 1, Appli
5	c	34	22.1	4411529	4	US-09-103-840A-1	Sequence 1, Appli
6	c	32.8	21.3	4403765	4	US-09-103-840A-2	Sequence 2, Appli
7	c	32.4	21.0	2238	1	US-07-841-651-1	Sequence 1, Appli
8	c	32.4	21.0	2238	1	US-07-841-651-1	Sequence 1, Appli
9	c	32	20.8	2119	3	US-09-032-372-6	Sequence 6, Appli
10	c	32	20.8	2119	3	US-09-032-372-6	Sequence 6, Appli
11	c	30.8	20.0	2787	4	US-09-105-537-40	Sequence 40, Appl
12	c	30.8	20.0	2787	4	US-09-105-537-40	Sequence 40, Appl
13	c	30.8	20.0	5970	3	US-09-320-878-21	Sequence 21, Appl
14	c	30.8	20.0	5970	3	US-09-320-878-21	Sequence 21, Appl
15	c	30.6	19.9	1734	6	5352575-8	Patent No. 5352575
16	c	30.6	19.9	1734	6	5352575-8	Patent No. 5352575
17	c	30.4	19.7	11219	1	US-07-642-734C-1	Sequence 1, Appli
18	c	30.4	19.7	11219	1	US-07-642-734C-1	Sequence 1, Appli
19	c	30.4	19.7	11219	3	US-08-439-009A-1	Sequence 1, Appli
20	c	30.4	19.7	11219	3	US-08-439-009A-1	Sequence 1, Appli
21	c	30.2	19.6	7898	4	US-08-984-709A-49	Sequence 49, Appl
22	c	30.2	19.6	7898	4	US-08-984-709A-49	Sequence 49, Appl
23	c	29.8	19.4	3252	2	US-08-809-740A-1	Sequence 1, Appli
24	c	29.8	19.4	3252	2	US-08-809-740A-1	Sequence 1, Appli
25	c	29.8	19.4	3252	2	US-08-809-740A-4	Sequence 4, Appli
26	c	29.8	19.4	3252	2	US-08-809-740A-4	Sequence 4, Appli
27	c	29.4	19.1	6822	4	US-09-426-998-3	Sequence 3, Appli
28	c	29.4	19.1	6822	4	US-09-426-998-3	Sequence 3, Appli
29	c	29.4	19.1	7741	4	US-09-426-998-4	Sequence 4, Appli
30	c	29	19.1	7741	4	US-09-426-998-4	Sequence 4, Appli
31		29	18.8	1790	4	US-09-133-962A-7	Sequence 7, Appli
32	c	28.8	18.8	1790	4	US-09-133-962A-7	Sequence 7, Appli
33	c	28.8	18.7	2335	4	US-09-387-574-9	Sequence 9, Appli
34	c	28.8	18.7	2335	4	US-09-387-574-9	Sequence 9, Appli
35	c	28.8	18.7	2335	4	US-09-668-096-9	Sequence 9, Appli
36	c	28.8	18.7	2335	4	US-09-668-096-9	Sequence 9, Appli
37	c	28.8	18.7	4848	4	US-08-955-957A-1	Sequence 1, Appli
38	c	28.8	18.7	4848	4	US-08-955-957A-1	Sequence 1, Appli
39	c	28.8	18.7	4848	4	US-08-955-957A-4	Sequence 4, Appli
40	c	28.8	18.7	4848	4	US-08-955-957A-4	Sequence 4, Appli
41	c	28.8	18.7	4848	4	US-08-955-957A-6	Sequence 6, Appli
42	c	28.8	18.7	4848	4	US-08-955-957A-6	Sequence 6, Appli
43	c	28.6	18.6	1296	1	US-07-816-283-9	Sequence 9, Appli
44	c	28.6	18.6	1296	1	US-07-816-283-9	Sequence 9, Appli
45	c	28.6	18.6	1296	1	US-08-417-103-9	Sequence 9, Appli

ALIGNMENTS

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RESULT 1
US-09-434-288-7
; Sequence 7, Application US/09434288
; Patent No. 6303767
; GENERAL INFORMATION:
;  APPLICANT: Betlach C., Melanie
;  APPLICANT: McDaniel, Robert
;  TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
;  TITLE OF INVENTION: CONSTRUCTS THEREFOR
;  FILE REFERENCE: 30062-20030.00
;  CURRENT APPLICATION NUMBER: US/09/434,288
;  CURRENT FILING DATE: 1999-11-05
;  PRIOR APPLICATION NUMBER: 60/107,093
;  PRIOR FILING DATE: 1998-11-05
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;  LENGTH: 1681
;  TYPE: DNA
;  ORGANISM: Streptomyces narbonensis
US-09-434-288-7

Query Match             22.6%;  Score 34.8;  DB 4;  Length 1681;
Best Local Similarity   55.9%;  Pred. No. 1.4;
Matches   66;  Conservative   0;  Mismatches   52;  Indels   0;  Gaps   0;

Qy      1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGGCGGAGCTGTCGTCATCTCGCT  60
            ||||| ||||||||| ||||| ||||| |||||| || |||| | ||||| ||||| |||
Db    424 CTGGCGCCGTGCTCAGCGGGCTCACCCGGCCGGCGGGGTCGCGGGCGCGGCCTCCGGTCGGC 483

Qy     61 CATCGTCGAGTCGGCGGCGCCGCCGACTCGACGATGACGAGATGACCAGCTCCGGCCGC  118
            | || ||||| |||| ||||| |  | ||||| | | |||  | |||| |||| || ||
Db    484 CGCCGCAGGGCCGGCCGCCGCACGCCGCCAGCGCCGCCGAGAGGGACCTCGGGCGGGCGGC  541

RESULT 2
US-09-434-288-7/c
; Sequence 7, Application US/09434288
; Patent No. 6303767
; GENERAL INFORMATION:
;  APPLICANT: Betlach C., Melanie
;  APPLICANT: McDaniel, Robert
;  TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
;  TITLE OF INVENTION: CONSTRUCTS THEREFOR
;  FILE REFERENCE: 30062-20030.00
;  CURRENT APPLICATION NUMBER: US/09/434,288
;  CURRENT FILING DATE: 1999-11-05
;  PRIOR APPLICATION NUMBER: 60/107,093
;  PRIOR FILING DATE: 1998-11-05
;  NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1681
; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-09-434-288-7

Query Match   22.6%;   Score 34.8; DB 4; Length 1681;
Best Local Similarity   55.9%;   Pred. No. 1.4;
Matches   66; Conservative   0; Mismatches   52; Indels   0; Gaps   0;

Qy   37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGCCGACTCGACGATGAG 96
           || || || ||||| ||| ||||| ||| || |||| || || || |
Db   541 GCCGCCGCCCAGGTCCCTCTCCGCCGGCGGTCCGTCGGCGGCGGCCCTGCGGCGGC 482

Qy   97 CGAGATGACCAGCTCGGCCGCCGCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
           | ||| || |||||||| ||||| |||| |||| || ||| ||| || ||
Db   481 CGACCGGAGCGCCGCCGCGCGCCGGGGTGAGCCCGCCGTGAGCAGCGGCGGCCAG 424

RESULT 3
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match   22.1%;   Score 34; DB 4; Length 4403765;
Best Local Similarity   59.2%;   Pred. No. 2.3;
Matches   58; Conservative   0; Mismatches   40; Indels   0; Gaps   0;

Qy   37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGCCGACTCGACGATGAG 96
           |||| ||| ||| || |||| | ||| |||||| | || || || || ||
Db 4251891 GCGGTGAAGATGATCACCACGCCCACCGACTGGCGCCGGCTACGGCGCTGGC 4251832

Qy   97 CGAGATGACCAGCTCCGGCCGCCGCGACTCGACGATGAGC 134
           | | |||| ||||| |||||| | | || || | ||
Db 4251831 CGGGGTGTCCAGCTTCGGCTTCGGCGGCGGCCAACGCGC 4251794

RESULT 4
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match   22.1%;   Score 34; DB 4; Length 4411529;
Best Local Similarity   59.2%;   Pred. No. 2.3;
Matches   58; Conservative   0; Mismatches   40; Indels   0; Gaps   0;

Qy   21 GCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCG 80
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Db 4259538 GCGGTTGGGCGCCGCCGAAGCGAAGCTGGACACCCGGCAGCGGCTAGCCGCCGTATC 4259597

Qy   81 CCGACTCACGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
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Db 4259598 GCGGCCAGTCGGTGGGCGGCGTGGTGATCATCTTCAACCGC 4259635

RESULT 5
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match   22.1%;   Score 34; DB 4; Length 4411529;
Best Local Similarity   59.2%;   Pred. No. 2.3;
Matches   58; Conservative   0; Mismatches   40; Indels   0; Gaps   0;

Qy   37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGCCGCCGACTCGACGATGAG 96
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Db 4259635 GCGGTTGAAGATGATCACCACGCCCACCGACTGGCGCCGGCTACGGCGCTGGC 4259576

Qy   97 CGAGATGACCAGCTCCGGCCGCCGCGACTCGACGATGAGC 134
           | || ||| || | |||| | || ||| || | | |
Db 4259575 CGGGGTGTCCAGCTTCGGCTTCGGCGGCGGCCAACGCGC 4259538

RESULT 6
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          21.3%;  Score 32.8;  DB 4;  Length 4403765;
Best Local Similarity 59.2%;  Pred. No.4.3;
Matches   58;  Conservative   0;  Mismatches   0;  Indels   40;  Gaps   0;

Qy        21 GCTCATCGTCGAGTCGGCGGCCGGCCGGGAGCTGGTCATCTGCTCATCCTCGTCATCGTCAGTCGGCGGCCG 80
             |||| ||||| || | ||  |||||| |||||||| |||| || || ||
Db   4251794 GCGCGGTTGGCGCCGCGAAGCCGGCCGGCGACACCCCGGCGCGTAGCCGCCGCGTATC 4251853

Qy        81 CCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
             || ||||| || || ||| ||| ||| |||| |||
Db   4251854 GCGGCCAGTCGGTGGGCGTGGTGATCATCTTCAACCGC 4251891

RESULT 7
US-07-841-651-1
; Sequence 1, Application US/07841651
; Patent No. 5410031
; GENERAL INFORMATION:
;     APPLICANT: Pajor, Ana M
;     APPLICANT: Wright, Ernest M
;     TITLE OF INVENTION: Cloning and Functional Expression of a
;     TITLE OF INVENTION: Mammalian Na+/Nucleoside Cotransporter: A Member of the
;     TITLE OF INVENTION: SGLT Family
;     NUMBER OF SEQUENCES: 4
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Sheldon & Mak
;        STREET: 225 South Lake Avenue, Ninth Floor
;        CITY: Pasadena
;        STATE: California
;        COUNTRY: USA
;        ZIP: 91101
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/07/841,651
;        FILING DATE: 19920224
;        CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Mandel, SaraLynn
;        REGISTRATION NUMBER: 31,853
;        REFERENCE/DOCKET NUMBER: 8772
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: (818) 796-4000
;        TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 2238 base pairs
;        TYPE: NUCLEIC ACID
;        STRANDEDNESS: double
;        TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     ORIGINAL SOURCE:
;        ORGANISM: Oryctolagus cuniculus
;     FEATURE:
;        NAME/KEY: CDS
;        LOCATION: 7..2022
US-07-841-651-1
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Query Match          21.0%;  Score 32.4;  DB 1;  Length 2238;
Best Local Similarity 62.2%;  Pred. No. 5.1;
Matches   51;  Conservative   0;  Mismatches   31;  Indels   0;  Gaps   0;

Qy        70 GTCGGCGGCCGGCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGA 129
             | ||| || || ||  || || || | ||||| ||  || |||| || |||||
Db       726 GACGGTGTCCGAGGACCCGGCTGTGGCAACATCTCCAGCTCCTGCTACCGACACCCGGCC 785

Qy       130 TGAGCGAGATGACCAGCTCCGG 151
             |||  | ||| || |||||||
Db       786 TGACTCCTATCATCTGCTCCGG 807

RESULT 8
US-07-841-651-1/C
; Sequence 1, Application US/07841651
; Patent No. 5410031
; GENERAL INFORMATION:
;     APPLICANT: Pajor, Ana M
;     APPLICANT: Wright, Ernest M
;     TITLE OF INVENTION: Cloning and Functional Expression of a
;     TITLE OF INVENTION: Mammalian Na+/Nucleoside Cotransporter: A Member of the
;     TITLE OF INVENTION: SGLT Family
;     NUMBER OF SEQUENCES: 4
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Sheldon & Mak
;        STREET: 225 South Lake Avenue, Ninth Floor
;        CITY: Pasadena
;        STATE: California
;        COUNTRY: USA
;        ZIP: 91101
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/07/841,651
;        FILING DATE: 19920224
;        CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Mandel, SaraLynn
;        REGISTRATION NUMBER: 31,853
;        REFERENCE/DOCKET NUMBER: 8772
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: (818) 796-4000
;        TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 2238 base pairs
;        TYPE: NUCLEIC ACID
;        STRANDEDNESS: double
;        TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     ORIGINAL SOURCE:
;        ORGANISM: Oryctolagus cuniculus
;     FEATURE:
;        NAME/KEY: CDS
;        LOCATION: 7..2022
US-07-841-651-1

Query Match          21.0%;  Score 32.4;  DB 1;  Length 2238;
Best Local Similarity 62.2%;  Pred. No. 5.1;
Matches   51;  Conservative   0;  Mismatches   31;  Indels   0;  Gaps   0;

Qy         4 CCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGCGAGCTGGTCATCTCGCTCAT 63
             |||||| || |||| || |||          ||  || ||  || |||| || || |||| ||
Db       807 CCGGAGCAGATGATAGGGAGTCAGGCCGGGGTCGGTCGGTAGCAGGAGAGCTGGAGATGTTGCCCAC 748

Qy        64 CGTCGAGTCGGCGGCCGGCGAC 85
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             | || ||| ||| ||| |||
Db   747 AGCCGGGGTCCTCGGACACCGTC 726
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RESULT 9
US-09-032-372-6
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
US-09-032-372-6

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Query Match       20.8%;     Score 32;  DB 3;   Length 2119;
Best Local Similarity    51.4%;    Pred. No. 6.4;
Matches   74;  Conservative   0;  Mismatches  70;  Indels   0;  Gaps   0;

Qy    5 CGGAGCTGGTCATCTGCGCTCATCGTGCGAGTCGGCGGCCGGGAGCTGGTCATCTCGCTCATC 64
          || ||| | | || |||    | ||||  || || |||  | |
Db  151 CGAGGCTCTCGCCTCTCCCGTCCGCTGCGTCCGCGCGGAAGATGGCAACCGAGGGGCTG 210

Qy   65 GTCGAGTCGGCGGCCGGGAGATGACGACTCGGCGCCGCCGACTC 124
          |||| | |  |||||    |||||||    ||   |||  ||
Db  211 CACGGAGAACGAGACGCTGGGCTCGTGAAGATGGCCGAGAGCCTCAAGGGCAAGCTG 270

Qy  125 GACGATGAGCGAGATGACCAGCTC 148
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Db  271 GAGGAGGAGCGGGAGAGCCTGCAC 294
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RESULT 10

US-09-032-372-6/c
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032,372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
US-09-032-372-6

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Query Match       20.8%;     Score 32;  DB 3;   Length 2119;
Best Local Similarity    51.4%;    Pred. No. 6.4;
Matches   74;  Conservative   0;  Mismatches  70;  Indels   0;  Gaps   0;

Qy    7 GAGCTGGTCATCTCGCTCATCGTCGCGAGTCGGCGGCCGGGAGCTGGTCATCTCGCTCATCGT 66
          ||| |||  ||    || | |||    |    || |||||||  |||  |||    ||
Db  294 GTGCAGCTTGGCTCGGCTCCTCCTCCCAGCTTGCCTTGCCTTGAGGCTCGGCCTCGCTCTTCAG 235

Qy   67 CGAGTCGGCGGCCGGGCCGCCGGCTCGGCGATGAGGCGAGATGACCAGCTCCGGCGCCGCCGACTCGA 126
          ||| | | | |||    | || | |||    ||  || ||| ||    ||| |||  | | ||
Db  234 CGACGCCAGCGTCGTTCTCGTTGCGAGCCCCTCGGTTGCCATCTTCGCGCGGGGACCCAG 175

Qy  127 CGATGAGCGAGATGACCAGCTCCG 150
          || || ||  || ||   |||  ||
Db  174 CGGAGAGGAAGCGGGAGAGCCTCG 151
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RESULT 11
US-09-105-537-40
; Sequence 40, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.

```
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT APPLICATION FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-40

Query Match          20.0%;    Score 30.8;   DB 4;   Length 2787;
Best Local Similarity 57.1%;   Pred. No.12;
Matches  56;  Conservative  0;  Mismatches 42;  Indels  0;  Gaps  0;

Qy  57 CGCTCATCGTCGAGTCGGCGGCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 116
        ||||| |||  ||| ||  ||  |||  |  ||||| || |||  ||| ||  ||
Db  77 CGCTCTTACTCGTCTCCGGACCGGCCGCAGCGGGAAGACGGAGCTGCTGCGGTCGCTCC 136

Qy 117 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
        ||||  ||  |||  ||||| |||  ||  ||||  ||
Db 137 GCCGGCTGGCCGCCGAGCGGGAGACCCCCGTCTGGTCG 174

RESULT 12
US-09-105-537-40/c
; Sequence 40, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT APPLICATION FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-40

Query Match          20.0%;    Score 30.8;   DB 4;   Length 2787;
Best Local Similarity 57.1%;   Pred. No.12;
Matches  56;  Conservative  0;  Mismatches 42;  Indels  0;  Gaps  0;

Qy   1 CGGCCGGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGCCGAGTCGGTCATCTCGCT 60
        || |||| ||  |||||||  ||  ||||||  ||||||||
Db 174 CGACCAGACGCGGGGGTCTCCCGCTCGGGGGCCCAGCCGCGGGAGCCGACCGCAGCAGCCGAGCTCCGT 115

Qy  61 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCG 98
        |  |||| |||  | |||  |||||  |||||
Db 114 CTTCCCGCTGCCCGGCCCGTCCGGAGACGAGTAAGAGCG 77

RESULT 13
US-09-320-878-21
; Sequence 21, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
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; FILE REFERENCE: 30622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 5970
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21

Query Match          20.0%;    Score 30.8;   DB 3;   Length 5970;
Best Local Similarity 57.1%;   Pred. No. 13;
Matches  56;  Conservative  0;  Mismatches 42;  Indels  0;  Gaps  0;

Qy   57 CGCTCATCGTCGAGTCGGCGGCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 116
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Db 2815 CGCTCTTACTCGTCTCCGGACCGGCCGCAGCGGGAAGACGGAGCTGCTGCGGTCGCTCC 2874

Qy  117 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
         ||||  ||  |||  ||||| |||  ||  ||||  ||
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RESULT 14
US-09-320-878-21/c
; Sequence 21, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 5970
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21

Query Match          20.0%;    Score 30.8;   DB 3;   Length 5970;
Best Local Similarity 57.1%;   Pred. No. 13;
Matches  56;  Conservative  0;  Mismatches 42;  Indels  0;  Gaps  0;
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Qy      1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60
            ||| ||| || ||  || |||||| ||| || ||||| ||||   |  |  ||  || |||
Db   2912 CGACCAGACGGGGGTCTCCCGCTCGGCGGCCAGCCGCCGGGAGCGACCGCGAGCAGCTCCGT 2853

Qy     61 CATCGTCGAGTCGGCGGCCGCCGGACTCGACGATGAGCG 98
            | ||   | ||||| | || ||| ||| | |||||
Db   2852 CTTCCCGCTGCCGGCCGCGGTCCGGAGACGAGTAAGAGCG 2815
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RESULT 15
5352575-8
;Patent No. 5352575
;   APPLICANT: PETROVSKIS, ERIK A.;POST, LEONARD E.;TIMMINS, JAMES G.
;   TITLE OF INVENTION: PSEUDORABIES VIRUS PROTEIN
;   NUMBER OF SEQUENCES: 12
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/513,282
;   FILING DATE: 20-APR-1990
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 100,817
;   FILING DATE: 29-JUN-1987
;   APPLICATION NUMBER: 886,260
;   FILING DATE: 16-JUL-1986
;   APPLICATION NUMBER: 784,787
;   FILING DATE: 04-OCT-1985
;   APPLICATION NUMBER: 801,799
;   FILING DATE: 26-NOV-1985
;   APPLICATION NUMBER: 844,113
;   FILING DATE: 26-MAR-1986
;SEQ ID NO:8:
;   LENGTH: 1734
5352575-8

  Query Match   19.9%; Score 30.6; DB 6; Length 1734;
  Best Local Similarity   51.9%; Pred. No. 14;
  Matches   69; Conservative   0; Mismatches   64; Indels   0; Gaps   0;

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Qy     22 CTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGGCGGCCGC 81
            |||  |  |  ||   || ||||||| |||||| || ||| ||| ||  |  | |||||| |
Db   1377 CTCGCGGCCGGTTCCGGGTGCCCACGCGGGGGGGGACGCCGCATGCTCTCGCCGGTGTACAC 1436

Qy     82 CGACTCGACGATGAGCGAGATGACCCAGCTCCGGCCGCCCGACTCGACGATGAGCGAGATGA 141
            | | ||| || ||||   |||| |  ||| |||||| | |||  |||||| ||| || | ||
Db   1437 CAGCCTGCCCACGCACGAGGACTACTACGACGCGGCACGACGACGACGAGCGAGGAGGCGGA 1496

Qy    142 CCAGCTCCGGCCG 154
            | | ||||| |
Db   1497 CGCCCGCCGGCGG 1509
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Search completed: November 19, 2002, 07:40:47
Job time : 8178 secs

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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        November 19, 2002, 04:53:30 ; Search time 29 Seconds
                                        (without alignments)
                                        2011.188 Million cell updates/sec

Title:           US-09-887-194A-13
Perfect score:   154
Sequence:        1 cggccggagctggtcatctc........gagatgaccagctccggccg 154

Scoring table:   IDENTITY_NUC
                 GapOp 10.0 , Gapext 1.0

Searched:        335578 seqs, 189365133 residues

Total number of hits satisfying chosen parameters:      671156

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		112	72.7	4974	9	US-09-906-209-17	Sequence 17, Appl
2	c	112	72.7	4974	9	US-09-906-209-17	Sequence 17, Appl
3		32.8	21.3	9210	9	US-09-712-363-100	Sequence 100, App
4	c	32.8	21.3	9210	9	US-09-712-363-100	Sequence 100, App
5		31.8	20.6	1573	10	US-09-822-830A-20	Sequence 20, Appl
6	c	31.8	20.5	1573	10	US-09-822-830A-20	Sequence 20, Appl
7		31.6	20.5	2451	10	US-09-815-242-7752	Sequence 7752, Ap
8	c	31.6	20.5	2451	10	US-09-815-242-7752	Sequence 7752, Ap
9		31.4	20.4	3202	10	US-09-954-456-210	Sequence 210, App
10	c	31.4	20.4	3202	10	US-09-954-456-210	Sequence 210, App
11		30.8	20.0	2787	9	US-09-860-846-40	Sequence 40, Appl
12	c	30.8	20.0	2787	9	US-09-860-846-40	Sequence 40, Appl
13		30.8	20.0	2787	10	US-09-861-289-40	Sequence 40, Appl
14	c	30.8	20.0	2787	10	US-09-861-289-40	Sequence 40, Appl
15		30.6	19.9	276	10	US-09-878-574-12270	Sequence 12270, A
16	c	30.6	19.9	276	10	US-09-878-574-12270	Sequence 12270, A
17		30.2	19.6	1533	9	US-09-712-363-81	Sequence 81, Appl
18	c	30.2	19.6	1533	9	US-09-712-363-81	Sequence 81, Appl
19		30	19.5	1536	10	US-09-815-242-4092	Sequence 4092, Ap
20	c	20	19.5	1536	10	US-09-815-242-4092	Sequence 4092, Ap
21	c	22	19.5	2280	10	US-09-822-830A-93	Sequence 93, Appl
22		22	30	2280	10	US-09-822-830A-93	Sequence 93, Appl
23	c	23	29.8	427	10	US-09-764-853-98	Sequence 98, Appl
24	c	24	29.8	427	10	US-09-764-853-98	Sequence 98, Appl
25		25	29.6	281	10	US-09-294-093B-171	Sequence 171, App
26	c	26	29.6	281	10	US-09-294-093B-171	Sequence 171, App
27		27	29.6	1575	9	US-09-712-363-78	Sequence 78, Appl
28	c	28	29.6	1575	9	US-09-712-363-78	Sequence 78, Appl
29		29	29.6	3042	9	US-09-712-363-68	Sequence 68, Appl
30	c	30	29.6	3042	9	US-09-712-363-68	Sequence 68, Appl
31		31	29.2	342	10	US-09-783-590-4679	Sequence 4679, Ap
32	c	32	29.2	342	10	US-09-783-590-4679	Sequence 4679, Ap
33	c	33	29.2	578	10	US-09-833-790-391	Sequence 391, App
34	c	34	29.2	578	10	US-09-833-790-391	Sequence 391, App
35		35	29.2	1100	10	US-09-867-550-1149	Sequence 1149, Ap
36	c	36	29.2	1100	10	US-09-867-550-1149	Sequence 1149, Ap
37		37	29.2	1610	10	US-09-880-107-2203	Sequence 2203, Ap
38	c	38	29.2	1610	10	US-09-880-107-2203	Sequence 2203, Ap
39		39	29.2	4139	10	US-09-880-107-2279	Sequence 2279, Ap
40	c	40	29.2	4139	10	US-09-880-107-2279	Sequence 2279, Ap
41		41	29	1066	9	US-09-764-868-390	Sequence 390, App
42	c	42	18.8	1066	9	US-09-764-868-390	Sequence 390, App
43	c	43	18.7	322	10	US-09-867-550-87	Sequence 87, Appl
44	c	44	28.8	322	10	US-09-867-550-87	Sequence 87, Appl
45	c	45	28.6	88421	9	US-09-976-059-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-906-209-17
; Sequence 17, Application US/09906209
; Patent No. US20020165385A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; APPLICANT: Carlson, Tom
; APPLICANT: Ilag, Lawrence L.
; TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
; FILE REFERENCE: BB1451 NA
; CURRENT APPLICATION NUMBER: US/09/906,209
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,712
; PRIOR FILING DATE: JULY 17, 2000
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 4974
; TYPE: DNA
; ORGANISM: synthetic construct
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3951)
; OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

Query Match   72.7%; Score 112; DB 9; Length 4974;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGACGATCGGCGGCCGGAGCTGGTCATCTCGCT 60
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Db   4863 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGACGATCGGCGGCCGGAGCTGGTCATCTCGCT 4922

Qy   61 CATCGTCGAGTCGGCGGCCGCCGACTCGACCATGAGCGAGATGACCAGCTCC 112
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RESULT 2
US-09-906-209-17/c

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; Sequence 17, Application US/09906209
; Patent No. US20020165385A1
; GENERAL INFORMATION:
;   APPLICANT: Allen, Steve
;   APPLICANT: Butler, Karla
;   APPLICANT: Carlson, Tom
;   APPLICANT: Ilag, Lawrence L.
;   TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
;   FILE REFERENCE: BB1451 NA
;   CURRENT APPLICATION NUMBER: US/09/906,209
;   CURRENT FILING DATE: 2001-07-16
;   PRIOR APPLICATION NUMBER: 60/218,712
;   PRIOR FILING DATE: JULY 17, 2000
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
;   LENGTH: 4974
;   TYPE: DNA
;   ORGANISM: synthetic construct
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3951)
;   OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

  Query Match           72.7%;  Score 112;  DB 9;  Length 4974;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-22;
  Matches  112;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4974 GGAGCTGGTCATCTCGCTCATCGTCCGAGTCGGCGGCGCCGCCCACTCGACGATGAGCGGAGAT 4915

Qy    103 GACCAGCTCCGGCCGCCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4914 GACCAGCTCCGGCCGCCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 4863


RESULT 3
US-09-712-363-100
; Sequence 100, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
;   APPLICANT: Eisenberg, David
;   APPLICANT: Rotstein, Sergio H.
;   APPLICANT: Marcotte, Edward M.
;   TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
;   TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
;   FILE REFERENCE: 07419-032001
;   CURRENT APPLICATION NUMBER: US/09/712,363
;   CURRENT FILING DATE: 2000-11-13
;   PRIOR APPLICATION NUMBER: PCT/US00/02246
;   PRIOR FILING DATE: 2000-01-28
;   PRIOR APPLICATION NUMBER: 60/179,531
;   PRIOR FILING DATE: 2000-02-01
;   PRIOR APPLICATION NUMBER: 60/117,844
;   PRIOR FILING DATE: 1999-01-29
;   PRIOR APPLICATION NUMBER: 60/118,206,
;   PRIOR FILING DATE: 1999-02-01
;   PRIOR APPLICATION NUMBER: 60/126,593
;   PRIOR FILING DATE: 1999-03-26
;   PRIOR APPLICATION NUMBER: 60/134,093
;   PRIOR FILING DATE: 1999-05-14
;   PRIOR APPLICATION NUMBER: 60/134,092
;   PRIOR FILING DATE: 1999-05-14
;   PRIOR APPLICATION NUMBER: 60/165,124
;   PRIOR FILING DATE: 1999-11-12
;   PRIOR APPLICATION NUMBER: 60/165,086
;   PRIOR FILING DATE: 1999-11-12
;   NUMBER OF SEQ ID NOS: 292
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
;   LENGTH: 9210
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-712-363-100

  Query Match           21.3%;  Score 32.8;  DB 9;  Length 9210;
  Best Local Similarity  59.8%;  Pred. No. 1.1;
  Matches  55;  Conservative  0;  Mismatches  37;  Indels  0;  Gaps  0;

Qy     36 GGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGCCGACTCGACGATGA 95
          |||-|| || |||| | ||||| | | ||||| || |-|||| || ||||| |- |||
Db   5966 GGCAGCTGGGACTGGACGACCCCGTCAACGCCCTTGCCGGCGCGCCGATTCCGAGCTGA 6025

Qy     96 GCGAGATGACCAGCTCCGGCCGCCGACTCGAC 127
          ||| ||   ||  ||||| | ||  | |||
Db   6026 TCGACTTGGTCACCGCCGAACTGGGAGCGGAC 6057


RESULT 4
US-09-712-363-100/c
; Sequence 100, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
;   APPLICANT: Eisenberg, David
;   APPLICANT: Rotstein, Sergio H.
;   APPLICANT: Marcotte, Edward M.
;   TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
;   TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
;   FILE REFERENCE: 07419-032001
;   CURRENT APPLICATION NUMBER: US/09/712,363
;   CURRENT FILING DATE: 2000-11-13
;   PRIOR APPLICATION NUMBER: PCT/US00/02246
;   PRIOR FILING DATE: 2000-01-28
;   PRIOR APPLICATION NUMBER: 60/179,531
;   PRIOR FILING DATE: 2000-02-01
;   PRIOR APPLICATION NUMBER: 60/117,844
;   PRIOR FILING DATE: 1999-01-29
;   PRIOR APPLICATION NUMBER: 60/118,206,
;   PRIOR FILING DATE: 1999-02-01
;   PRIOR APPLICATION NUMBER: 60/126,593
;   PRIOR FILING DATE: 1999-03-26
;   PRIOR APPLICATION NUMBER: 60/134,093
;   PRIOR FILING DATE: 1999-05-14
;   PRIOR APPLICATION NUMBER: 60/134,092
;   PRIOR FILING DATE: 1999-05-14
;   PRIOR APPLICATION NUMBER: 60/165,124
;   PRIOR FILING DATE: 1999-11-12
;   PRIOR APPLICATION NUMBER: 60/165,086
;   PRIOR FILING DATE: 1999-11-12
;   NUMBER OF SEQ ID NOS: 292
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
;   LENGTH: 9210
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
US-09-712-363-100

  Query Match           21.3%;  Score 32.8;  DB 9;  Length 9210;
  Best Local Similarity  59.8%;  Pred. No. 1.1;
  Matches  55;  Conservative  0;  Mismatches  37;  Indels  0;  Gaps  0;

Qy     28 GTCGAGTCGGCCGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGCCGACTC 87
          ||| || ||| ||| || ||||| || |||| | | ||||| || ||||| || |-|||
Db   6057 GTCCGCTCCCAGTTGCGGGTGACCAGCTCCGGGTGACCAGCTCGATCAGCTCGGAATCGGGG 5998

Qy     88 GACGATGAGCGAGATGACCAGCTCCGGCCGCC 119
          | ||||||| || | |||  ||||| || |||
Db   5997 GGCGTTGACGGGGTCGTCCAGTCCAGCTGCC 5966


RESULT 5
US-09-822-830A-20
; Sequence 20, Application US/09822830A
; Patent No. US20020142952A1
```

```
; GENERAL INFORMATION:
;   APPLICANT: Genetics Institute, Inc.
;   APPLICANT: Wong, Gordon G.
;   APPLICANT: Clark, Hilary
;   APPLICANT: Fechtel, Kim
;   APPLICANT: Agostino, Michael J.
;   APPLICANT: Howes, Steven H.
;   APPLICANT: Resnick, Richard J.
;   APPLICANT: Gulukota, Kamalakar
;   APPLICANT: Graham, James R.
;   TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
;   FILE REFERENCE: GIN 6402
;   CURRENT APPLICATION NUMBER: US/09/822,830A
;   CURRENT FILING DATE: 2001-03-29
;   PRIOR APPLICATION NUMBER: 60/195,604
;   PRIOR FILING DATE: 2000-04-06
;   NUMBER OF SEQ ID NOS: 631
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 1573
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-822-830A-20

Query Match             20.6%;  Score 31.8;  DB 10;  Length 1573;
Best Local Similarity   54.8%;  Pred. No. 1.7;
Matches   63;  Conservative   0;  Mismatches  52;  Indels   0;  Gaps   0;

Qy    37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAG  96
         || |||||  |||| |  | |  | | |||||| || | ||||||| ||| || | |||
Db    68 GCCACCGCCGCTGCTGCGCTGCTCGTGTTGGCGTCGCCCTCCGGCGCCGTC 127

Qy    97 CGAGATGACCAGCTCCGGCCCCGGCCCCGACTCGACGATGAGCGAGATGACCAGCTCCGG 151
         ||     | |||| || || || || || |  | |||||| ||  | |||||| |||||
Db   128 CGCCCCGATCCCTTCGCCCCGCCAGCTGGGGACACGCAGAACTGCCAGCTGCGG 182

RESULT 6
US-09-822-830A-20/c
; Sequence 20, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
;   APPLICANT: Genetics Institute, Inc.
;   APPLICANT: Wong, Gordon G.
;   APPLICANT: Clark, Hilary
;   APPLICANT: Fechtel, Kim
;   APPLICANT: Agostino, Michael J.
;   APPLICANT: Howes, Steven H.
;   APPLICANT: Resnick, Richard J.
;   APPLICANT: Gulukota, Kamalakar
;   APPLICANT: Graham, James R.
;   TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
;   FILE REFERENCE: GIN 6402
;   CURRENT APPLICATION NUMBER: US/09/822,830A
;   CURRENT FILING DATE: 2001-03-29
;   PRIOR APPLICATION NUMBER: 60/195,604
;   PRIOR FILING DATE: 2000-04-06
;   NUMBER OF SEQ ID NOS: 631
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 1573
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-822-830A-20

Query Match             20.6%;  Score 31.8;  DB 10;  Length 1573;
Best Local Similarity   54.8%;  Pred. No. 1.7;
Matches   63;  Conservative   0;  Mismatches  52;  Indels   0;  Gaps   0;

Qy     4 CCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCGGCCGCCGAGCTGGTCATCTCGCTCAT  63
         ||| |||||  | |  | || |||| |||| || |||||||| || |
Db   182 CCGCAGCTGGCAGTTCTGCGTGTCCCCGAGCTGGGCGGCCGGAAGGGATCGCGGGCGGACGG 123
```

```
Qy    64 CGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
         || ||| |||| |||||| ||||| | ||  | | ||| ||| |||||| ||| ||
Db   122 CGCGGAGGCGGGGGGCGGGGCGGCGGAGCCCAACAGCAGCAGCAGCGGCGCGGTGGC  68
```

```
RESULT 7
US-09-815-242-7752
; Sequence 7752, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
;   TITLE OF INVENTION: Identification of Essential Genes in
;   TITLE OF INVENTION: Prokaryotes
;   FILE REFERENCE: ELITRA.011A
;   CURRENT APPLICATION NUMBER: US/09/815,242
;   CURRENT FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/191,078
;   PRIOR FILING DATE: 2000-03-21
;   PRIOR APPLICATION NUMBER: 60/206,848
;   PRIOR FILING DATE: 2000-05-23
;   PRIOR APPLICATION NUMBER: 60/207,727
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: 60/242,578
;   PRIOR FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: 60/253,625
;   PRIOR FILING DATE: 2000-11-27
;   PRIOR APPLICATION NUMBER: 60/257,931
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: 60/269,308
;   PRIOR FILING DATE: 2001-02-16
;   NUMBER OF SEQ ID NOS: 14110
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7752
;   LENGTH: 2451
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(2451)
US-09-815-242-7752

Query Match             20.5%;  Score 31.6;  DB 10;  Length 2451;
Best Local Similarity   62.8%;  Pred. No. 2;
Matches   49;  Conservative   0;  Mismatches  29;  Indels   0;  Gaps   0;

Qy    43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGAT 102
         ||||||||||||||||||| || ||||||   || | ||| || |||||||||
Db  1398 GGAACAGATCCTGATCAGCACCGTCGGCGGCCGCGCCGCCGACGTCAAGCCGAAGAGCGAGAA 1457

Qy   103 GACCAGCTCCGGCGCCG 120
         | |||| |||  |||| ||
Db  1458 GGCCATCTGCGGCTGCAG 1475

RESULT 8
US-09-815-242-7752/c
; Sequence 7752, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
```

; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210.
;   LENGTH: 3202
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-210

Query Match   20.4%;   Score 31.4; DB 10;   Length 3202;
Best Local Similarity   64.4%;   Pred. No. 2.3;
Matches   47; Conservative   0; Mismatches   26; Indels   0; Gaps   0;

Qy   35 CGGCGGCCGGAGCTGGTCATCCTGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATG 94
           || | ||||||| || ||||||| ||| ||||||| ||||||| | |||| |||| |
Db   1494 CGGCAGGCCGAGCTGGACAGCGAGCTCATCATCGAGTCGTCGCGACGCCTCCTCGGCCTCG 1553

Qy   95 AGCGAGATGACCA 107
           |||| |||
Db   1554 GAGGAGAGCCCCA 1566

RESULT 10
US-09-954-456-210/c
; Sequence 210, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;   APPLICANT: Young, Paul
;   TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
;   TITLE OF INVENTION: Sets
;   FILE REFERENCE: 689290-76
;   CURRENT APPLICATION NUMBER: US/09/954,456
;   CURRENT FILING DATE: 2001-09-18
;   PRIOR APPLICATION NUMBER: US/60/233,617
;   PRIOR FILING DATE: 2000-09-18
;   PRIOR APPLICATION NUMBER: US/60/234,052
;   PRIOR FILING DATE: 2000-09-20
;   PRIOR APPLICATION NUMBER: US/60/234,923
;   PRIOR FILING DATE: 2000-09-25
;   PRIOR APPLICATION NUMBER: US/60/235,134
;   PRIOR FILING DATE: 2000-09-25
;   PRIOR APPLICATION NUMBER: US/60/235,637
;   PRIOR FILING DATE: 2000-09-26
;   PRIOR APPLICATION NUMBER: US/60/235,638
;   PRIOR FILING DATE: 2000-09-26
;   PRIOR APPLICATION NUMBER: US/60/235,711
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: US/60/235,720
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: US/60/235,840
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: US/60/235,863
;   PRIOR FILING DATE: 2000-09-27
;   NUMBER OF SEQ ID NOS: 2276
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210
;   LENGTH: 3202
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-210

Query Match   20.4%;   Score 31.4; DB 10;   Length 3202;
Best Local Similarity   64.4%;   Pred. No. 2.3;
Matches   47; Conservative   0; Mismatches   26; Indels   0; Gaps   0;

Qy   48 TGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCA 107
           ||| ||||| ||||| |||| |||||| |||||||| | | ||| ||| ||| ||||||
Db   1566 TGGGCCTCTCCTCCGAGGCCGAGGAGGCGTCGCACGACTCGATGATGAGCTCGCTGTCCA 1507

Qy   108 GCTCCGGCCGCCG 120
           |||| |||
Db   1506 GCTCGGCCTCGCG 1494

; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7752
;   LENGTH: 2451
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(2451)
US-09-815-242-7752

Query Match   20.5%;   Score 31.6; DB 10;   Length 2451;
Best Local Similarity   62.8%;   Pred. No. 2;
Matches   49; Conservative   0; Mismatches   29; Indels   0; Gaps   0;

Qy   35 CGGCGGCCGGAGCTGGTCATCCTGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATG 94
           | || |||||| ||| ||||||| |||||| | | || |||| | |||||| ||
Db   1475 CTGCAGCCGCAGATGGCCTTCTCGCCTCTTCGCGTTGACGTCGGCCGCGGCGGCCCACGTG 1416

Qy   95 AGCGAGATGACCAGCTCC 112
           |||| ||||
Db   1415 CTGATCAGGATCTGTTCC 1398

RESULT 9
US-09-954-456-210
; Sequence 210, Application US/09954456
; Patent No. US2002011505701A1
; GENERAL INFORMATION:
;   APPLICANT: Young, Paul
;   TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;   TITLE OF INVENTION: Sets
;   FILE REFERENCE: 689290-76
;   CURRENT APPLICATION NUMBER: US/09/954,456
;   CURRENT FILING DATE: 2001-09-18
;   PRIOR APPLICATION NUMBER: US/60/233,617
;   PRIOR FILING DATE: 2000-09-18
;   PRIOR APPLICATION NUMBER: US/60/234,052
;   PRIOR FILING DATE: 2000-09-20
;   PRIOR APPLICATION NUMBER: US/60/234,923
;   PRIOR FILING DATE: 2000-09-25
;   PRIOR APPLICATION NUMBER: US/60/235,134
;   PRIOR FILING DATE: 2000-09-25
;   PRIOR APPLICATION NUMBER: US/60/235,637
;   PRIOR FILING DATE: 2000-09-26
;   PRIOR APPLICATION NUMBER: US/60/235,638
;   PRIOR FILING DATE: 2000-09-26
;   PRIOR APPLICATION NUMBER: US/60/235,711
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: US/60/235,720
;   PRIOR FILING DATE: 2000-09-27
;   PRIOR APPLICATION NUMBER: US/60/235,840
;   PRIOR FILING DATE: 2000-09-27

RESULT 11
US-09-860-846-40
; Sequence 40, Application US/09860846
; Patent No. US2002164742A1
; GENERAL INFORMATION:
;   APPLICANT: Sherman, D.H.
;   APPLICANT: Liu, H.
;   APPLICANT: Xue, Y.
;   APPLICANT: Zhao, L.
;   TITLE OF INVENTION: DNA encoding methymycin and pikromycin
;   FILE REFERENCE: 600.438US1
;   CURRENT APPLICATION NUMBER: US/09/860,846
;   CURRENT FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: 09/105,537
;   PRIOR FILING DATE: 1998-06-26
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 40
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Streptomyces venezuelae
US-09-860-846-40

Query Match   20.0%; Score 30.8; DB 9; Length 2787;
Best Local Similarity   57.1%; Pred. No. 3.3;
Matches   56; Conservative   0; Mismatches 42; Indels   0; Gaps   0;

Qy   57 CGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 116
              ||||| ||| || | || |||| ||||||| ||| || || |||||
Db   77 CGCTCTTACTCGTCTCCGGACGCCGGCGGCCAGCGGGAAGACGGAGCTGCTGCGGTCGCTCC 136

Qy   117 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
              |||| ||| || ||||| || || || ||
Db   137 GCCGGCTGGCCCGCAGCGGGAGACCCCCGTCTGTCG 174

RESULT 12
US-09-860-846-40/c
; Sequence 40, Application US/09860846
; Patent No. US2002164742A1
; GENERAL INFORMATION:
;   APPLICANT: Sherman, D.H.
;   APPLICANT: Liu, H.
;   APPLICANT: Xue, Y.
;   APPLICANT: Zhao, L.
;   TITLE OF INVENTION: DNA encoding methymycin and pikromycin
;   FILE REFERENCE: 600.438US1
;   CURRENT APPLICATION NUMBER: US/09/860,846
;   CURRENT FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: 09/105,537
;   PRIOR FILING DATE: 1998-06-26
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 40
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Streptomyces venezuelae
US-09-860-846-40

Query Match   20.0%; Score 30.8; DB 9; Length 2787;
Best Local Similarity   57.1%; Pred. No. 3.3;
Matches   56; Conservative   0; Mismatches 42; Indels   0; Gaps   0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGGAGCTGTCATCTCGCT 60
              ||||| ||| || || |||||| | || |||||| || || |||| | ||
Db   174 CGACCAGACGGGGTCTCCCCGTCCCGGCGGCCAGCCGCGGCGACCGCCAGCAGCTCCGT 115

Qy   61 CATCGTCGAGTCGGCGCGCCGCCCGACTCGACGATGAGCG 98
              || ||| ||||| | |||| | || ||| ||||||
Db   114 CTTCCCGCGTCCCGGCCGGGTCCGGAGACGAGTAAGAGCG 77

RESULT 13
US-09-861-289-40
; Sequence 40, Application US/09861289
; Patent No. US2002110897A1
; GENERAL INFORMATION:
;   APPLICANT: Sherman, D.H.
;   APPLICANT: Liu, H.
;   APPLICANT: Xue, Y.
;   APPLICANT: Zhao, L.
;   TITLE OF INVENTION: DNA encoding methymycin and pikromycin
;   FILE REFERENCE: 600.438US1
;   CURRENT APPLICATION NUMBER: US/09/861,289
;   CURRENT FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: 09/105,537
;   PRIOR FILING DATE: 1998-06-26
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 40
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Streptomyces venezuelae
US-09-861-289-40

Query Match   20.0%; Score 30.8; DB 10; Length 2787;
Best Local Similarity   57.1%; Pred. No. 3.3;
Matches   56; Conservative   0; Mismatches 42; Indels   0; Gaps   0;

Qy   57 CGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 116
              ||||| ||| || | || |||| ||||||| ||| || || |||||
Db   77 CGCTCTTACTCGTCTCCGGACGCCGGCGGCCAGCGGGAAGACGGAGCTGCTGCGGTCGCTCC 136

Qy   117 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
              |||| ||| || ||||| || || || ||
Db   137 GCCGGCTGGCCCGCAGCGGGAGACCCCCGTCTGGTCG 174

RESULT 14
US-09-861-289-40/c
; Sequence 40, Application US/09861289
; Patent No. US2002110897A1
; GENERAL INFORMATION:
;   APPLICANT: Sherman, D.H.
;   APPLICANT: Liu, H.
;   APPLICANT: Xue, Y.
;   APPLICANT: Zhao, L.
;   TITLE OF INVENTION: DNA encoding methymycin and pikromycin
;   FILE REFERENCE: 600.438US1
;   CURRENT APPLICATION NUMBER: US/09/861,289
;   CURRENT FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: 09/105,537
;   PRIOR FILING DATE: 1998-06-26
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   SEQ ID NO 40
;   LENGTH: 2787
;   TYPE: DNA
;   ORGANISM: Streptomyces venezuelae
US-09-861-289-40

Query Match   20.0%; Score 30.8; DB 10; Length 2787;
Best Local Similarity   57.1%; Pred. No. 3.3;
Matches   56; Conservative   0; Mismatches 42; Indels   0; Gaps   0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGGAGCTGTCATCTCGCT 60
              ||||| ||| || || |||||| | || |||||| || || |||| | ||
Db   174 CGACCAGACGGGGTCTCCCCGTCCCGGCGGCCAGCCGCGGCGACCGCCAGCAGCTCCGT 115

Qy   61 CATCGTCGAGTCGGCGCGCCGCCCGACTCGACGATGAGCG 98
              || ||| ||||| | |||| | || ||| ||||||
Db   114 CTTCCCGCGTCCCGGCCGGGTCCGGAGACGAGTAAGAGCG 77

RESULT 15
US-09-878-574-12270
; Sequence 12270, Application US/09878574
; Patent No. US2002011054BA1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 12270
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701065564H1
US-09-878-574-12270

Query Match   19.9%;   Score 30.6; DB 10;   Length 276;
Best Local Similarity   60.0%;   Pred. No. 3.2;
Matches   51; Conservative   0; Mismatches   34;   Indels   0;   Gaps   0;

Qy   51 TCATCTCGCTCATCGTCGGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCT 110
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Db   150 TCCTCTTCCTCATCCTCTTAGTGGCGCTCTTCCCCTCGTCGCTCGCTCCGAGATCCGCTTCT 209

Qy   111 CCGGCCGCCGACTCGACGATGAGCG 135
         ||| |||| |||| |||||||| ||
Db   210 CCGAGATCCGAAACGACGACGATCCGCCG 234

Search completed: November 19, 2002, 05:26:35
Job time : 46 secs

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OM nucleic - nucleic search, using sw model

              GenCore version 5.1.3
         Copyright (c) 1993 - 2002 Compugen Ltd.

Run on:       November 19, 2002, 05:22:26 ; Search time 3509 Seconds
                                    (without alignments)
                                    1103.432 Million cell updates/sec

Title:         US-09-887-194A-13
Perfect score: 154
Sequence:      1 cggccggagctggtcatctc.........gagatgaccagctccggccg 154

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      24791104 seqs, 1257243825 residues

Total number of hits satisfying chosen parameters:          49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		154	100.0	154	33	US-09-887-194A-13	Sequence 13, Appl
2	c	154	100.0	154	33	US-09-887-194A-13	Sequence 13, Appl
3		154	100.0	154	35	US-09-934-900-25	Sequence 25, Appl
4	c	154	100.0	154	35	US-09-934-900-25	Sequence 25, Appl
5		154	100.0	154	65	US-60-213-961-13	Sequence 13, Appl
6	c	154	100.0	154	65	US-60-213-961-13	Sequence 13, Appl
7		112	72.7	4974	34	US-09-906-209-17	Sequence 17, Appl
8	c	112	72.7	4974	34	US-09-906-209-17	Sequence 17, Appl
9		82.8	53.8	6611	35	US-09-934-900-26	Sequence 26, Appl
10	c	82.8	53.8	6611	35	US-09-934-900-26	Sequence 26, Appl
11		81	52.6	963	33	US-09-887-194A-29	Sequence 29, Appl
12	c	81	52.6	963	33	US-09-887-194A-29	Sequence 29, Appl
13		80	51.9	80	33	US-09-887-194A-12	Sequence 12, Appl
14	c	80	51.9	80	33	US-09-887-194A-12	Sequence 12, Appl
15		80	51.9	80	35	US-09-934-900-24	Sequence 24, Appl
16	c	80	51.9	80	35	US-09-934-900-24	Sequence 24, Appl
17		80	51.9	80	65	US-60-213-961-12	Sequence 12, Appl
18	c	80	51.9	80	65	US-60-213-961-12	Sequence 12, Appl
19		80	51.9	92	33	US-09-887-194A-14	Sequence 14, Appl
20	c	80	51.9	92	33	US-09-887-194A-14	Sequence 14, Appl
21	c	80	51.9	92	65	US-60-213-961-14	Sequence 14, Appl

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c 22  51.9  80    92    65  US-60-213-961-14        Sequence 14, Appl
c 23  29.7  45.8  1717  33  US-09-887-194A-24       Sequence 24, Appl
c 24  29.7  45.8  1717  33  US-09-887-194A-24       Sequence 24, Appl
c 25  24.8  38.2  2297  52  US-60-082-302-335       Sequence 335, App
c 26  24.8  38.2  2297  52  US-60-082-302-335       Sequence 335, App
c 27  24.0  37    1501  31  US-09-815-264-4004      Sequence 4004, Ap
c 28  24.0  37    1501  31  US-09-815-264-4004      Sequence 4004, Ap
c 29  24.0  37    1576  24  US-09-620-392-67826     Sequence 67826, A
c 30  24.0  37    1576  24  US-09-620-392-67826     Sequence 67826, A
c 31  24.0  37    3437  28  US-09-702-134-8908      Sequence 8908, Ap
c 32  24.0  37    3437  28  US-09-702-134-8908      Sequence 8908, Ap
c 33  24.0  37    3437  31  US-09-815-264-81901     Sequence 81901, A
c 34  24.0  37    3437  31  US-09-815-264-81901     Sequence 81901, A
c 35  24.0  37    3450  24  US-09-620-392-25325     Sequence 25325, A
c 36  24.0  37    3450  24  US-09-620-392-25325     Sequence 25325, A
c 37  23.6  36.4  437   63  US-60-197-872-30118     Sequence 30118, A
c 38  23.6  36.4  437   63  US-09-620-392-30118     Sequence 30118, A
c 39  23.6  36.4  680   25  US-09-654-617-390937    Sequence 390937,
c 40  23.6  36.4  680   25  US-09-654-617-390937    Sequence 390937,
c 41  23.6  36.4  680   27  US-09-684-016-390937    Sequence 390937,
c 42  23.6  36.4  680   27  US-09-684-016-390937    Sequence 390937,
c 43  23.6  36.4  3799  24  US-09-620-392-54439     Sequence 54439, A
c 44  23.6  36.4  3799  24  US-09-620-392-54439     Sequence 54439, A
c 45  23.6  36.4  3799  28  US-09-702-134-20957     Sequence 20957, A
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ALIGNMENTS

RESULT 1
US-09-887-194A-13
; Sequence 13, Application US/09887194A
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BB1449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-09-887-194A-13

Query Match   100.0%; Score 154; DB 33; Length 154;
Best Local Similarity   100.0%; Pred. No. 6.7e-25;
Matches 154; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60

Qy   61 CATCGTCGAGTCGGCGGCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGTCGAGTCGGCGGCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 120

Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
         ||||||||||||||||||||||||||||||||||
Db  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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RESULT 2
US-09-887-194A-13/c

Sequence 13, Application US/09887194A
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRES:
; FILE REFERENCE: BB1449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementar:
; OTHER INFORMATION: region of pKS133
US-09-887-194A-13

Query Match   100.0%; Score 154; DB 33; Length 154;
Best Local Similarity   100.0%; Pred. No. 6.7e-25;
Matches 154; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 CATCGTCGAGTCGGCGGCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 120
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Db   94 CATCGTCGAGTCGGCGGCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 35

Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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Db   34 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 1
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RESULT 3
US-09-934-900-25
; Sequence 25, Application US/09934900
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stea:
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-09-934-900-25

Query Match   100.0%; Score 154; DB 35; Length 154;
Best Local Similarity   100.0%; Pred. No. 6.7e-25;
Matches 154; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   61 CATCGTCGAGTCGGCGGCCGGCCCGGCCGCCGGAGCGAGCGAGCGAGATGACCAGCTCCGGCGCCG  120
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RESULT 4
US-09-934-900-25/c
; Sequence 25, Application US/09934900
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl
; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:   ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
US-09-934-900-25

Query Match          100.0%;  Score 154;  DB 35;  Length 154;
Best Local Similarity 100.0%;  Pred. No. 6.7e-25;
Matches 154;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   61 CATCGTCGAGTCGGCGGCCGGCCCGGCCGCCGGAGCGAGCGAGATGACCAGCTCCGGCGCCG  120
        ||||||||||||||||||||||||||||||||||
Db   94 CATCGTCGAGTCGGCGGCCGGCCCGGCCGCCGGAGCGAGATGACCAGCTCCGGCGCCG  35
Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154
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Db   34 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  1

RESULT 5
US-60-213-961-13
; Sequence 13, Application US/60213961
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: BB1449 US PRV
; CURRENT APPLICATION NUMBER: US/60/213,961
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
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;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:   ELVISLIVES complementa
;   OTHER INFORMATION: region of pKS133
US-60-213-961-13

Query Match          100.0%;  Score 154;  DB 65;  Length 154;
Best Local Similarity 100.0%;  Pred. No. 6.7e-25;
Matches 154;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db    1 CGGCCCGAGCTGGTCATCTCGCTCATCGTCCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60
Qy   61 CATCGTCGAGTCGGCGGCCGGCCCGGCCGCCGGAGCGAGCGAGATGACCAGCTCCGGCGCCG  120
        |||||||||||||||||||||||||||||||||||||||
Db   61 CATCGTCGAGTCGGCGGCCGGCCCGGCCGCCGGAGCGAGCGAGATGACCAGCTCCGGCGCCG  120
Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154
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Db  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154

RESULT 6
US-60-213-961-13/c
; Sequence 13, Application US/60213961
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPR
; FILE REFERENCE: BB1449 US PRV
; CURRENT APPLICATION NUMBER: US/60/213,961
; CURRENT FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:   ELVISLIVES complementa
;   OTHER INFORMATION: region of pKS133
US-60-213-961-13

Query Match          100.0%;  Score 154;  DB 65;  Length 154;
Best Local Similarity 100.0%;  Pred. No. 6.7e-25;
Matches 154;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 CGGCCCGAGCTGGTCATCTCGCTCATCGTCCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  154 CGGCCCGAGCTGGTCATCTCGCTCATCGTCCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  95
Qy   61 CATCGTCGAGTCGGCGGCCGGCCCGGCCGCCGGAGCGAGCGAGATGACCAGCTCCGGCGCCG  120
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db   94 CATCGTCGAGTCGGCGGCCGGCCCGGCCGCCGGAGCGAGCGAGATGACCAGCTCCGGCGCCG  35
Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154
        |||||||||||||||||||||
Db   34 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  1

RESULT 7
US-09-906-209-17
; Sequence 17, Application US/09906209
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Butler, Karla
; APPLICANT: Carlson, Tom
```

; APPLICANT: Ilag, Lawrence L.
; TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
; FILE REFERENCE: BB1451 NA
; CURRENT APPLICATION NUMBER: US/09/906,209
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,712
; PRIOR FILING DATE: JULY 17, 2000
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
;   LENGTH: 4974
;   TYPE: DNA
;   ORGANISM: synthetic construct
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3951)
;   OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

Query Match   72.7%; Score 112; DB 34; Length 4974;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCAGTCGTCGGCGGCCGGAGCTGGTCATCTCGCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4863 CGGCCGGAGCTGGTCATCTCGCTCAGTCGTCGGCGGCCGGAGCTGGTCATCTCGCT 4922

Qy   61 CATCGTCGAGTCGGCGGCGGCCGGACTCGACGATGAGCGAGATGACCAGCTCC 112
          |||||||||||||||||||||||||||||||||||||||||||
Db 4923 CATCGTCGAGTCGGCGGCGGCCGGACTCGACGATGAGCGAGATGACCAGCTCC 4974

RESULT 8
US-09-906-209-17/c
; Sequence 17, Application US/09906209
; GENERAL INFORMATION:
;   APPLICANT: Allen, Steve
;   APPLICANT: Butler, Karla
;   APPLICANT: Carlson, Tom
;   APPLICANT: Ilag, Lawrence L.
;   TITLE OF INVENTION: Plastidic Phosphoglucomutase Genes
;   FILE REFERENCE: BB1451 NA
;   CURRENT APPLICATION NUMBER: US/09/906,209
;   CURRENT FILING DATE: 2001-07-16
;   PRIOR APPLICATION NUMBER: 60/218,712
;   PRIOR FILING DATE: JULY 17, 2000
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
;   LENGTH: 4974
;   TYPE: DNA
;   ORGANISM: synthetic construct
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3951)
;   OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17/c

Query Match   72.7%; Score 112; DB 34; Length 4974;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   43 GGAGCTGGTCATCTCGCTCAGTCGTCGGCGGCCGGAGCTGGTCATGCGAGCGAGAT 102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4974 GGAGCTGGTCATCTCGCTCAGTCGTCGGCGGCCGGAGCTGGTCATGCGAGCGAGAT 4915

Qy   103 GACCAGCTCCGGCGGCCGCCGGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
          |||||||||||||||||||||||||||||||||||||||||||||
Db 4914 GACCAGCTCCGGCGGCCGCCGGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 4863

RESULT 9
US-09-934-900-26

; Sequence 26, Application US/09934900
; GENERAL INFORMATION:
;   APPLICANT: Booth, Russ
;   APPLICANT: Cahoon, Rebecca E
;   APPLICANT: Hitz, William D
;   APPLICANT: Kinney, Anthony
;   APPLICANT: Yadav, Naren
;   TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stea
;   TITLE OF INVENTION: ACP Desaturase
;   FILE REFERENCE: BB1476 US NA
;   CURRENT APPLICATION NUMBER: US/09/934,900
;   CURRENT FILING DATE: 2001-08-22
;   PRIOR APPLICATION NUMBER: 60/226996
;   PRIOR FILING DATE: 2000-08-22
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
;   LENGTH: 6611
;   TYPE: DNA
;   ORGANISM: Plasmid pBS68
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: (4436)..(4436)
;   OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

Query Match   53.8%; Score 82.8; DB 35; Length 6611;
Best Local Similarity 97.7%; Pred. No. 3.8e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCTCGCTCATCTCGCTCGGCGGCCGGAGCTGGTCATCTCGCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5348 CGGCCGGAGCTGGTCATCTCGCTCATCTCGCTCATCTCGCTCGGCGGCCGGAGCTGGTCATCTCGCT 5407

Qy   61 CATCGTCGAGTCGGCGGCGGCCGGACT 86
          ||||||||||||||||||||||| ||
Db 5408 CATCGTCGAGTCGGCGGCGGCCGCTGAGT 5433

RESULT 10
US-09-934-900-26/c
; Sequence 26, Application US/09934900
; GENERAL INFORMATION:
;   APPLICANT: Booth, Russ
;   APPLICANT: Cahoon, Rebecca E
;   APPLICANT: Hitz, William D
;   APPLICANT: Kinney, Anthony
;   APPLICANT: Yadav, Naren
;   TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stea
;   TITLE OF INVENTION: ACP Desaturase
;   FILE REFERENCE: BB1476 US NA
;   CURRENT APPLICATION NUMBER: US/09/934,900
;   CURRENT FILING DATE: 2001-08-22
;   PRIOR APPLICATION NUMBER: 60/226996
;   PRIOR FILING DATE: 2000-08-22
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
;   LENGTH: 6611
;   TYPE: DNA
;   ORGANISM: Plasmid pBS68
;   FEATURE:
;   NAME/KEY: Unsure
;   LOCATION: (4436)..(4436)
;   OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

Query Match   53.8%; Score 82.8; DB 35; Length 6611;
Best Local Similarity 97.7%; Pred. No. 3.8e-09;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy   69 AGTCGCGGCCGCCGGACTCGACGATGAGCGAGATGACCAGCTCCGGCGGCCGGACTCGACG 128
          | || ||||||||||||||||||||||||||||||||||||||||

Db 5433 ACTCAGCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 5374

Qy   129 ATGAGGGAGATGACCAGCTCCGGCCG 154
          ||||||||||||||||||||||||||
Db 5373 ATGAGCGAGATGACCAGCTCCGGCCG 5348

RESULT 11
US-09-887-194A-29
; Sequence 29, Application US/09887194A
; GENERAL INFORMATION:
;   APPLICANT: Glassman, Kimberly F.
;   APPLICANT: Gordon-Kamm, William J.
;   APPLICANT: Kinney, Anthony
;   APPLICANT: Lowe, Keith S.
;   APPLICANT: Nichols, Scott E.
;   APPLICANT: Stecca, Kevin L.
;   TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
;   FILE REFERENCE: BB1449 US NA
;   CURRENT APPLICATION NUMBER: US/09/887,194A
;   CURRENT FILING DATE: 2002-03-13
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
;   LENGTH: 963
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
;   OTHER INFORMATION: region of pKS149
US-09-887-194A-29

Query Match   52.6%; Score 81; DB 33; Length 963;
Best Local Similarity   100.0%; Pred. No. 1.1e-08;
Matches   81; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   74 GCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGCCGACTCGACGATGAG 133
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 883 GCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGCCGACTCGACGATGAG 942

Qy 134 CGAGATGACCAGCTCCGGCCG 154
         |||||||||||||||||||||
Db 943 CGAGATGACCAGCTCCGGCCG 963

RESULT 12
US-09-887-194A-29/c
; GENERAL INFORMATION:
;   APPLICANT: Glassman, Kimberly F.
;   APPLICANT: Gordon-Kamm, William J.
;   APPLICANT: Kinney, Anthony
;   APPLICANT: Lowe, Keith S.
;   APPLICANT: Nichols, Scott E.
;   APPLICANT: Stecca, Kevin L.
;   TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
;   FILE REFERENCE: BB1449 US NA
;   CURRENT APPLICATION NUMBER: US/09/887,194A
;   CURRENT FILING DATE: 2002-03-13
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
;   LENGTH: 963
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
;   OTHER INFORMATION: region of pKS149
US-09-887-194A-29

Query Match   52.6%; Score 81; DB 33; Length 963;
Best Local Similarity   100.0%; Pred. No. 1.1e-08;
Matches   81; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCGGGCCGGAGCTGGTCATCTCGCT 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 963 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCGGGCCGGAGCTGGTCATCTCGCT 904

Qy   61 CATCGTCGAGTCGGCGGCCGC 81
         |||||||||||||||||||||
Db 903 CATCGTCGAGTCGGCGGCCGC 883

RESULT 13
US-09-887-194A-12
; Sequence 12, Application US/09887194A
; GENERAL INFORMATION:
;   APPLICANT: Glassman, Kimberly F.
;   APPLICANT: Gordon-Kamm, William J.
;   APPLICANT: Kinney, Anthony
;   APPLICANT: Lowe, Keith S.
;   APPLICANT: Nichols, Scott E.
;   APPLICANT: Stecca, Kevin L.
;   TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRE
;   FILE REFERENCE: BB1449 US NA
;   CURRENT APPLICATION NUMBER: US/09/887,194A
;   CURRENT FILING DATE: 2002-03-13
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
;   LENGTH: 80
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementa
;   OTHER INFORMATION: region of pKS106 and pKS124
US-09-887-194A-12

Query Match   51.9%; Score 80; DB 33; Length 80;
Best Local Similarity   100.0%; Pred. No. 2.3e-08;
Matches   80; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   38 CGGCCGGAGCTGGTCATCGTCATCGTCGAGTCGCGGGCCGGAGCTGGTCATCGTCGACGATGAGC 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGGCCGGAGCTGGTCATCGTCATCGTCGAGTCGCGGGCCGGAGCTGGTCATCGTCGACGATGAGC 60

Qy   98 GAGATGACCAGCTCCGGCCG 117
         ||||||||||||||||||||
Db   61 GAGATGACCAGCTCCGGCCG 80

RESULT 14
US-09-887-194A-12/c
; Sequence 12, Application US/09887194A
; GENERAL INFORMATION:
;   APPLICANT: Glassman, Kimberly F.
;   APPLICANT: Gordon-Kamm, William J.
;   APPLICANT: Kinney, Anthony
;   APPLICANT: Lowe, Keith S.
;   APPLICANT: Nichols, Scott E.
;   APPLICANT: Stecca, Kevin L.
;   TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRE
;   FILE REFERENCE: BB1449 US NA
;   CURRENT APPLICATION NUMBER: US/09/887,194A
;   CURRENT FILING DATE: 2002-03-13
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
;   LENGTH: 80
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementa
;   OTHER INFORMATION: region of pKS106 and pKS124
US-09-887-194A-12

```
Query Match          51.9%;   Score 80;   DB 33;   Length 80;
Best Local Similarity 100.0%;  Pred. No. 2.3e-08;
Matches  80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    80 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 21

Qy    98 GAGATGACCAGCTCCGGCCG 117
         ||||||||||||||||||||
Db    20 GAGATGACCAGCTCCGGCCG 1
```

RESULT 15
US-09-934-900-24

```
; Sequence 24, Application US/09934900
; GENERAL INFORMATION:
;  APPLICANT: Booth, Russ
;  APPLICANT: Cahoon, Rebecca E
;  APPLICANT: Hitz, William D
;  APPLICANT: Kinney, Anthony
;  APPLICANT: Yadav, Naren
;  TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
;  TITLE OF INVENTION:  ACP Desaturase
;  FILE REFERENCE: BB1476 US NA
;  CURRENT APPLICATION NUMBER: US/09/934,900
;  CURRENT FILING DATE:  2001-08-22
;  PRIOR APPLICATION NUMBER: 60/226996
;  PRIOR FILING DATE: 2000-08-22
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
;  LENGTH: 80
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:  ELVISLIVES complementary
;  OTHER INFORMATION: region of pks106 and pks124
US-09-934-900-24
```

```
Query Match          51.9%;   Score 80;   DB 35;   Length 80;
Best Local Similarity 100.0%;  Pred. No. 2.3e-08;
Matches  80;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 97
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGC 60

Qy    98 GAGATGACCAGCTCCGGCCG 117
         ||||||||||||||||||||
Db    61 GAGATGACCAGCTCCGGCCG 80
```

Search completed: November 19, 2002, 06:28:11
Job time : 3532 secs

```
                    GenCore version 5.1.3
            Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     November 19, 2002, 05:19:28 ; Search time 126 Seconds
                                         (without alignments)
                                         229.391 Million cell updates/sec

Title:      US-09-887-194A-13
Perfect score: 154
Sequence:   1 cggccggagctggtcatctc.........gagatgaccagctccggccg 154

Scoring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

Searched:   224397 seqs, 93841606 residues

Total number of hits satisfying chosen parameters:        448794

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   .Pending_Patents_NA_New:*
             1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
             2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
             3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
             4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
             5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
             6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
             7: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		34.8	22.6	1681	6	US-10-271-889-7	Sequence 7, Appli
2	c	34.8	22.6	1681	6	US-10-271-889-7	Sequence 7, Appli
3		33	21.4	345	5	US-09-513-999C-8640	Sequence 8640, Ap
4	c	33	21.4	345	5	US-09-513-999C-8640	Sequence 8640, Ap
5	c	31.4	20.4	1707	6	US-10-267-255-68	Sequence 68, Appl
6	c	31.4	20.4	1707	6	US-10-267-255-68	Sequence 68, Appl
7		31.4	20.4	53500	6	US-10-267-255-76	Sequence 76, Appl
8	c	31.4	20.4	53500	6	US-10-267-255-76	Sequence 76, Appl
9	c	30.8	20.0	2787	6	US-10-271-889-40	Sequence 40, Appl
10	c	30.8	20.0	2787	6	US-10-271-889-40	Sequence 40, Appl
11	c	28.4	18.4	3284	6	US-10-240-425-1526	Sequence 1526, Ap
12	c	28.4	18.4	3284	6	US-10-240-425-1526	Sequence 1526, Ap
13	c	28.4	18.4	11220	6	US-10-271-889-32	Sequence 32, Appl
14	c	28.4	18.4	11220	6	US-10-271-889-32	Sequence 32, Appl
15	c	28.4	18.4	36778	6	US-10-271-889-48	Sequence 48, Appl
16	c	28.4	18.4	36778	6	US-10-271-889-48	Sequence 48, Appl
17	c	27.4	17.8	1030	6	US-10-240-425-1427	Sequence 1427, Ap
18	c	27.4	17.8	1030	6	US-10-240-425-1427	Sequence 1427, Ap
19	c	27.4	17.8	1419	6	US-10-267-255-61	Sequence 61, Appl
20	c	27.4	17.8	1419	6	US-10-267-255-61	Sequence 61, Appl
21	c	27.4	17.8	2327	1	PCT-US02-33723-66	Sequence 66, Appl
22	c	27.4	17.8	2327	1	PCT-US02-33723-66	Sequence 66, Appl
23	c	27.2	17.7	658	6	US-10-209-582-181	Sequence 181, App
24	c	27.2	17.7	658	6	US-10-209-582-181	Sequence 181, App
25	c	27.2	17.7	795	6	US-10-267-255-57	Sequence 57, Appl
26	c	27.2	17.7	795	6	US-10-267-255-57	Sequence 57, Appl
27		26.8	17.4	813	6	US-10-267-255-29	Sequence 29, Appl
28	c	26.8	17.4	813	6	US-10-267-255-29	Sequence 29, Appl
29		26.8	17.4	18331	6	US-10-267-255-96	Sequence 96, Appl
30	c	26.8	17.4	18331	6	US-10-267-255-96	Sequence 96, Appl
31		26.6	17.3	195	5	US-09-513-999C-13979	Sequence 13979, A
32	c	26.6	17.3	195	5	US-09-513-999C-13979	Sequence 13979, A
33		26.6	17.3	505	6	US-10-240-425-1014	Sequence 1014, Ap
34	c	26.6	17.3	505	6	US-10-240-425-1014	Sequence 1014, Ap
35		26.6	17.3	3517	6	US-10-257-022-20	Sequence 20, Appl
36	c	26.6	17.3	3517	6	US-10-257-022-20	Sequence 20, Appl
37		26.6	17.3	4689	6	US-10-271-889-34	Sequence 34, Appl
38	c	26.6	17.3	4689	6	US-10-271-889-34	Sequence 34, Appl
39		26.6	17.3	5180	6	US-10-152-319A-2042	Sequence 2042, Ap
40	c	26.6	17.3	5180	6	US-10-152-319A-2042	Sequence 2042, Ap
41		26.4	17.1	354	6	US-10-285-876-6	Sequence 6, Appli
42	c	26.4	17.1	354	6	US-10-285-876-6	Sequence 6, Appli
43		26.4	17.1	1766	6	US-10-240-425-1548	Sequence 1548, Ap
44	c	26.4	17.1	1766	6	US-10-240-425-1548	Sequence 1548, Ap
45	c	26.4	17.1	1984	7	US-60-419-986-3	Sequence 3, Appli

ALIGNMENTS

```
RESULT 1
US-10-271-889-7
; Sequence 7, Application US/10271889
; GENERAL INFORMATION:
;  APPLICANT: Sherman, D.H.
;  APPLICANT: Liu, H.
;  APPLICANT: Xue, Y.
;  APPLICANT: Zhao, L.
;  TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
;  FILE REFERENCE: 600.582US1
;  CURRENT APPLICATION NUMBER: US/10/271,889
;  CURRENT FILING DATE: 2002-10-15
;  PRIOR APPLICATION NUMBER: US 09/861,289
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 09/860,846
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 09/836,821
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: US 09/105,537
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;  LENGTH: 1681
;  TYPE: DNA
;  ORGANISM: Streptomyces narbonensis
US-10-271-889-7

    Query Match             22.6%;  Score 34.8;  DB 6;  Length 1681;
    Best Local Similarity   55.9%;  Pred. No. 0.26;
    Matches   66;  Conservative  0;  Mismatches  52;  Indels  0;  Gaps  0;

Qy    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCGGAGCTGGTCATCTCGCT 60
          ||  ||  |||||||| ||| ||  |  ||  |  |||||  |||||| | |  ||  || |
Db  424 CTGGCGCCGCTCGTCAGCGGGCTCACCCGCGGTCGCCGGCGGCGTCCGGCGTCGGTCGGC 483

Qy   61 CATCGTCGAGTCGGCGGCCCGGCGCCGGCCGACGCCCGGCCGCGCTGGGCGGGCGGCGGC 118
          ||  |  |   |  ||  ||  |   |   |||||||||||| | |   | |  |  ||  ||
Db  484 CGCCGCCAGGGCGGCGGCGGCGACGGCGGCGGCCGGGCGGGCGGCGGCGGCGGCGGCGGC 541

RESULT 2
US-10-271-889-7/c
; Sequence 7, Application US/10271889
; GENERAL INFORMATION:
;  APPLICANT: Sherman, D.H.
;  APPLICANT: Liu, H.
;  APPLICANT: Xue, Y.
;  APPLICANT: Zhao, L.
```

; TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
; FILE REFERENCE: 600.582US1
; CURRENT APPLICATION NUMBER: US/10/271,889
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US-09/861,289
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 09/860,846
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 09/836,821
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1681
;   TYPE: DNA
;   ORGANISM: Streptomyces narbonensis
US-10-271-889-7

Query Match   22.6%;   Score 34.8; DB 6; Length 1681;
Best Local Similarity   55.9%;   Pred. No. 0.26;
Matches   66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy   37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGCCGACTCGACGATGAG 96
          || ||| | ||| | |||||| | || | | |||| ||| | ||||| | |||| | |
Db   541 GCCGCCCGCCCAGGTCCCTCCTCCGCCGGTGCCCGTGCCGTCGGCGGCGGCCCTGCGGCGGC 482

Qy   97 CGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGGCAGATGACCAGCTCCGGCCG 154
          || || | | | || | | || || ||| | |||| ||| | | |||| |||| |
Db   481 CGACCGGAGGCGCCGCCGCCCGCCCGCGACCCGCGGTGAGCCCGGTGAGCGCAGCGGCCCAG 424

RESULT 3
US-09-513-999C-8640
; Sequence 8640, Application US/09513999C
; GENERAL INFORMATION:
;   APPLICANT: Dumas Milne Edwards, J.B.
;   APPLICANT: Duclert, A.
;   APPLICANT: Giordano, J.Y.
;   TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;   FILE REFERENCE: 59.US2.REG
;   CURRENT APPLICATION NUMBER: US/09/513,999C
;   CURRENT FILING DATE: 2000-02-24
;   PRIOR APPLICATION NUMBER: US 60/122,487
;   PRIOR FILING DATE: 1999-02-26
;   NUMBER OF SEQ ID NOS: 36681
;   SOFTWARE: Patent.pm
; SEQ ID NO 8640
;   LENGTH: 345
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 73
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 319
;   OTHER INFORMATION: y=c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 320
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 321
;   OTHER INFORMATION: y=c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 336
;   OTHER INFORMATION: k=g or t
;   FEATURE:

; NAME/KEY: misc_feature
;   LOCATION: 345
;   OTHER INFORMATION: m=a or c
US-09-513-999C-8640

Query Match   21.4%;   Score 33; DB 5; Length 345;
Best Local Similarity   62.3%;   Pred. No. 0.58;
Matches   48; Conservative 2; Mismatches 27; Indels 0; Gaps 0;

Qy   3 GCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCGCCGGAGCTGGTCATCTCGCTCA 62
          ||| || |||||||| |||||| | ||||| | ||| || |||| ||| |||||||||||
Db   246 GCCCGACGTGGTCATTTCTCTCACCACCACCGGCTACCGCCCGACGTGGTCCTTTCCCTCA 305

Qy   63 TCGTCGAGTCGGCGGCC 79
          | || | || | ::|
Db   306 CCACCCAGCCTACYKYC 322

RESULT 4
US-09-513-999C-8640/c
; Sequence 8640, Application US/09513999C
; GENERAL INFORMATION:
;   APPLICANT: Dumas Milne Edwards, J.B.
;   APPLICANT: Duclert, A.
;   APPLICANT: Giordano, J.Y.
;   TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
;   FILE REFERENCE: 59.US2.REG
;   CURRENT APPLICATION NUMBER: US/09/513,999C
;   CURRENT FILING DATE: 2000-02-24
;   PRIOR APPLICATION NUMBER: US 60/122,487
;   PRIOR FILING DATE: 1999-02-26
;   NUMBER OF SEQ ID NOS: 36681
;   SOFTWARE: Patent.pm
; SEQ ID NO 8640
;   LENGTH: 345
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 73
;   OTHER INFORMATION: n=a, g, c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 319
;   OTHER INFORMATION: y=c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 320
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 321
;   OTHER INFORMATION: y=c or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 336
;   OTHER INFORMATION: k=g or t
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 345
;   OTHER INFORMATION: m=a or c
US-09-513-999C-8640

Query Match   21.4%;   Score 33; DB 5; Length 345;
Best Local Similarity   62.3%;   Pred. No. 0.58;
Matches   48; Conservative 2; Mismatches 27; Indels 0; Gaps 0;

Qy   76 GGGCCGCCGACTCGACGATCGAGCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGCCGCCGACTCGACGATGAGCG 135
          |::: || | ||| | |||| ||| |||| | | | |||||| | ||| | ||||| |||| |||
Db   322 GRMRGTAGGCTGGCGGTGGTGAGGAAAAGGACCACGTCGGGCGGTAGGCTGGGGTGGTGAGAG 263

Qy   136 AGATGACCAGCTCCGGC 152
          | ||||||| || ||||

us-09-887-194a-13.rnpn

Db   262 AAATGACCACGTCGGGC 246

RESULT 5
US-10-267-255-68
; Sequence 68, Application US/10267255
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 68
;   LENGTH: 1707
;   TYPE: DNA
;   ORGANISM: Streptomyces lavendulae
US-10-267-255-68

Query Match   20.4%; Score 31.4; DB 6; Length 1707;
Best Local Similarity   56.2%; Pred. No. 2.1;
Matches   59; Conservative   0; Mismatches   46; Indels   0; Gaps   0;

Qy   46 GCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGCCGACTCGACGATGAGCGAGATGAC 105
             ||||||||| ||| ||| |||| | |||||||| |||| | ||||||| ||| | |
Db   666 GCGGTTCTTCATGTGCATGATCCAGAACCCGGGGTTCGACGGGCGGGTGATGGAGCTCAA 725

Qy   106 CAGCTCCGGCCGCCGACTCCGACGATGAGCGAGATGACCAGCTCCG 150
             || | |||||| ||| |||| |||||| |||| ||| | |||
Db   726 CACCCCGGGCCGCCGCTGGTGCGCCGCGGTGGGACTACGCACCCGGCCCG 770

RESULT 6
US-10-267-255-68/c
; Sequence 68, Application US/10267255
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 68
;   LENGTH: 1707
;   TYPE: DNA
;   ORGANISM: Streptomyces lavendulae
US-10-267-255-68

Query Match   20.4%; Score 31.4; DB 6; Length 1707;
Best Local Similarity   56.2%; Pred. No. 2.1;
Matches   59; Conservative   0; Mismatches   46; Indels   0; Gaps   0;

Qy   5 CGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGCCGAGCTGGTCATCTCGCTCATC 64
             ||| |||| |||| ||| | | ||| | |||||| | |||| ||| | ||||| || |||
Db   770 CGGGCCGGTCGTCGTAGTCCACCGCCGCCACCAGCCGCCGCCGGGTGTTGAGCTCCATCACC 711

Qy   65 GTCGAGTCGGCGGCGCCGACTCGACGATGAGCGAGATGACCAGC 109
             | | |||| ||| ||| || || ||| ||| ||| | |
Db   710 GCCCCGTCGAACCCGGGGTTCTGGATCATGCACATGAAGAAACCGC 666

RESULT 7
US-10-267-255-76
; Sequence 76, Application US/10267255
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
;   LENGTH: 53500
;   TYPE: DNA
;   ORGANISM: Streptomyces lavendulae
US-10-267-255-76

RESULT 8
US-10-267-255-76/c
; Sequence 76, Application US/10267255
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/624,447
; PRIOR FILING DATE: 1996-08-19

Query Match   20.4%; Score 31.4; DB 6; Length 53500;
Best Local Similarity   56.2%; Pred. No. 3.9;
Matches   59; Conservative   0; Mismatches   46; Indels   0; Gaps   0;

Qy   46 GCTGGTCATCTCGCTCATCGTCGAGTCGGCCGCCGCCGACTCGACGATGAGCGAGATGAC 105
             ||| ||||| ||| ||| |||| | |||||||| |||| | ||||||| ||| | |
Db   46289 GCGGTTCTTCATGTGCATGATCCAGAACCCGGGGTTCGACGGGCGGGTGATGGAGCTCAA 46348

Qy   106 CAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCG 150
             || | |||||| ||| |||| |||||| |||| ||| | |||
Db   46349 CACCCCGGGCCGCCGCTGGTGCGCCGCGGTGGGACTACGCACCCGGCCCCG 46393

```
;   PRIOR APPLICATION NUMBER: PCT/US94/11279
;   PRIOR FILING DATE: 1994-10-06
;   PRIOR APPLICATION NUMBER: US 08/133,963
;   PRIOR FILING DATE: 1993-10-07
;   SOFTWARE: FastSEQ for Windows Version 3.0
;   NUMBER OF SEQ ID NOS: 145
;   SEQ ID NO 76
;   LENGTH: 53500
;   TYPE: DNA
;   ORGANISM: Streptomyces lavendulae
US-10-267-255-76

Query Match       20.4%;  Score 31.4; DB 6; Length 53500;
Best Local Similarity   56.2%;  Pred. No. 3.9;
Matches    59; Conservative    0; Mismatches    46; Indels    0; Gaps    0;

Qy       5 CGGAGCTGGTCATCTCGCTCATCGCTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATC 64
             ||| )  ||| | ||| |  | ||||| |||||||| | |||||| | |||||||||||
Db   46393 CGGGCCGGTCGTGAGTCCACCGCGGCCACCAGCGGCGGCCCGGGCGTGTTGAGCTCCATCACC 46334

Qy      65 GTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGC 109
             | | |||| |||   ||| ||| ||| |||  | ||| | |||
Db   46333 GCCCCGTCGAAACCCCGGGTTCTGGATCATGCACATGAAGAACCGC 46289

RESULT 9
US-10-271-889-40
;  Sequence 40, Application US/10271889
;  GENERAL INFORMATION:
;  APPLICANT: Sherman, D.H.
;  APPLICANT: Liu, H.
;  APPLICANT: Xue, Y.
;  APPLICANT: Zhao, L.
;  TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
;  FILE REFERENCE: 600.582US1
;  CURRENT APPLICATION NUMBER: US/10/271,889
;  CURRENT FILING DATE: 2002-10-15
;  PRIOR APPLICATION NUMBER: US 09/861,289
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 09/860,846
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 09/836,821
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: US 09/105,537
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 40
;  LENGTH: 2787
;  TYPE: DNA
;  ORGANISM: Streptomyces venezuelae
US-10-271-889-40

Query Match       20.0%;  Score 30.8; DB 6; Length 2787;
Best Local Similarity   57.1%;  Pred. No. 3.3;
Matches    56; Conservative    0; Mismatches    42; Indels    0; Gaps    0;

Qy      57 CGCTCATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCC 116
             ||||| | ||| || | ||||||  | |||| || | ||| || |||||| || ||
Db      77 CGCTCTTACTCGTCTCCGGAACCGCGGCCGCCGGGAAGACCGAGCTGCTGCGGGTCGCTCC 136

Qy     117 GCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
             ||||| ||  |||| || ||  || || ||
Db     137 GCCGGCTGGCCCGAGCGGGAGACCCCCGTCTGGTCG 174

RESULT 10
US-10-271-889-40/c
;  Sequence 40, Application US/10271889
;  GENERAL INFORMATION:
;  APPLICANT: Sherman, D.H.
;  APPLICANT: Liu, H.
;  APPLICANT: Xue, Y.
```

```
;  APPLICANT: Zhao, L.
;  TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
;  FILE REFERENCE: 600.582US1
;  CURRENT APPLICATION NUMBER: US/10/271,889
;  CURRENT FILING DATE: 2002-10-15
;  PRIOR APPLICATION NUMBER: US 09/861,289
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 09/860,846
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 09/836,821
;  PRIOR FILING DATE: 2001-04-17
;  PRIOR APPLICATION NUMBER: US 09/105,537
;  PRIOR FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 40
;  LENGTH: 2787
;  TYPE: DNA
;  ORGANISM: Streptomyces venezuelae
US-10-271-889-40

Query Match       20.0%;  Score 30.8; DB 6; Length 2787;
Best Local Similarity   57.1%;  Pred. No. 3.3;
Matches    56; Conservative    0; Mismatches    42; Indels    0; Gaps    0;

Qy       1 CGGCCGGAGCTGGTCATCTCGCTCATCGCTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60
             || | ||| || |  ||||| ||||||  | | ||||| ||||||| |||||||||||
Db     174 CGACCAGACGGGGGTCTCCCGCTCGGCGGCCGCCGGGCGGCCGAGCGACCGGCAGCAGCTCCGGT 115

Qy      61 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGCG 98
             || || |  || ||  ||||| ||| || ||| ||||
Db     114 CTTCCCGCTGCCGGCCGGTCCGGAGACGAGTAAGAGCG 77

RESULT 11
US-10-240-425-1526
;  Sequence 1526, Application US/10240425
;  GENERAL INFORMATION:
;  APPLICANT: Williams, Amanda
;  APPLICANT: Boland, Joseph F.
;  APPLICANT: Lord, Reginald V.
;  APPLICANT: Alvarez, Chris
;  APPLICANT: Wetzel, Jon C.
;  APPLICANT: Scherf, Uwe
;  APPLICANT: Vockley, Joseph G.
;  TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;  FILE REFERENCE: 44921-5026
;  CURRENT APPLICATION NUMBER: US/10/240,425
;  CURRENT FILING DATE: 2002-09-30
;  PRIOR APPLICATION NUMBER: PCT/US01/09847
;  PRIOR FILING DATE: 2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/193,446
;  PRIOR FILING DATE: 2000-03-31
;  NUMBER OF SEQ ID NOS: 1588
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 1526
;  LENGTH: 3284
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: Genbank Accession No. X02344
US-10-240-425-1526

Query Match       18.4%;  Score 28.4; DB 6; Length 3284;
Best Local Similarity   54.9%;  Pred. No. 15;
Matches    56; Conservative    0; Mismatches    46; Indels    0; Gaps    0;

Qy       1 CGGCCGGAGCTGGTCATCTCGCTCATCGCTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT 60
             |||| |||  |  | ||||| ||||||  | ||||||| || ||||| ||||||||
Db     657 CGGACGGTCGGTTAGCACTCTGCGGCCGCCCGCTCTTCGCTCGTCGTTGTCTACTTCCT 716

Qy      61 CATCGTCGAGTCGGCGGCCGCCGACTCGACGATGAGGGAT 102
             | || || ||  |||| ||||| || ||  || |||
```

Db   717 CCTCTTCCCGCGCGCGCCGCCGCCGCCATCATGAGGGAAAT 758

RESULT 12
US-10-240-425-1526/c
; Sequence 1526, Application US/10240425
; GENERAL INFORMATION:
;   APPLICANT: Williams, Amanda
;   APPLICANT: Boland, Joseph F.
;   APPLICANT: Lord, Reginald V.
;   APPLICANT: Alvarez, Chris
;   APPLICANT: Wetzel, Jon C.
;   APPLICANT: Scherf, Uwe
;   APPLICANT: Vockley, Joseph G.
;   TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
;   FILE REFERENCE: 44921-5026
;   CURRENT APPLICATION NUMBER: US/10/240,425
;   CURRENT FILING DATE: 2002-09-30
;   PRIOR APPLICATION NUMBER: PCT/US01/09847
;   PRIOR FILING DATE: 2001-03-28
;   PRIOR APPLICATION NUMBER: US 60/193,446
;   PRIOR FILING DATE: 2000-03-31
;   NUMBER OF SEQ ID NOS: 1588
;   SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1526
;   LENGTH: 3284
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. X02344
US-10-240-425-1526

Query Match   18.4%; Score 28.4; DB 6; Length 3284;
Best Local Similarity 54.9%; Pred. No.15;
Matches   56; Conservative   0; Mismatches   46; Indels   0; Gaps   0;

Qy   53 ATCTGCTCATCGTCGAGTGGCGGCGCCGACTCGACGATGAGCGAGATGACCAGCTCC 112
            || |||| ||| |-| ||||||| ||- |||| ||| ||-|||||| |
Db   758 ATTTCCCTCATGATGGCGGCGCGCGGCGGCGGGGAAGAGGAAGTAGACAAAACAGC 699

Qy   113 GGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
            ||| || ||| ||| ||||| ||| ||| |
Db   698 AGCAAGAGCGGGGCGCGCAGAGTGCTACAACCGACCGTCCG 657

RESULT 13
US-10-271-889-32
; Sequence 32, Application US/10271889
; GENERAL INFORMATION:
;   APPLICANT: Sherman, D.H.
;   APPLICANT: Liu, H.
;   APPLICANT: Xue, Y.
;   APPLICANT: Zhao, L.
;   TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
;   FILE REFERENCE: 600.582US1
;   CURRENT APPLICATION NUMBER: US/10/271,889
;   CURRENT FILING DATE: 2002-10-15
;   PRIOR APPLICATION NUMBER: US 09/861,289
;   PRIOR FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: US 09/860,846
;   PRIOR FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: US 09/836,821
;   PRIOR FILING DATE: 2001-04-17
;   PRIOR APPLICATION NUMBER: US 09/105,537
;   PRIOR FILING DATE: 1998-06-26
;   NUMBER OF SEQ ID NOS: 55
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 11220
;   TYPE: DNA
;   ORGANISM: Streptomyces venezuelae
US-10-271-889-32

Query Match   18.4%; Score 28.4; DB 6; Length 11220;
Best Local Similarity 52.5%; Pred. No.18;
Matches   62; Conservative   0; Mismatches   56; Indels   0; Gaps   0;

Qy   37 GCGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGACTCGACGATGAG 96
            || ||| ||| |||| ||| ||||||| || |||||| || |||||||| ||||| |||
Db   10560 GCTGGCCGCCGCTGCTCAGCGGGCTCACCCGGATCGCGGTCGGCGGCGGCCGGTCAA 10619

Qy   97 CGAGATGACCAGCTCCGGCCGCCGCCGCCGCCGCACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
            | |- ||| ||| | |||| | |-||| | |||| |||| |
Db   10620 CCAGCGCAGGGCAGCCGCCGGAGGCGCGGGAGCGCGGGACACGGACCTCCGCCGGCGCGG 10677

RESULT 14
US-10-271-889-32/c
; Sequence 32, Application US/10271889
; GENERAL INFORMATION:
;   APPLICANT: Sherman, D.H.
;   APPLICANT: Liu, H.
;   APPLICANT: Xue, Y.
;   APPLICANT: Zhao, L.
;   TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
;   FILE REFERENCE: 600.582US1
;   CURRENT APPLICATION NUMBER: US/10/271,889
;   CURRENT FILING DATE: 2002-10-15
;   PRIOR APPLICATION NUMBER: US 09/861,289
;   PRIOR FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: US 09/860,846
;   PRIOR FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: US 09/836,821
;   PRIOR FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: US 09/105,537
;   PRIOR FILING DATE: 1998-06-26
;   NUMBER OF SEQ ID NOS: 55
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 11220
;   TYPE: DNA
;   ORGANISM: Streptomyces venezuelae
US-10-271-889-32

Query Match   18.4%; Score 28.4; DB 6; Length 11220;
Best Local Similarity 52.5%; Pred. No.18;
Matches   62; Conservative   0; Mismatches   56; Indels   0; Gaps   0;

Qy   1 CGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGAGCTGGTCATCTCGCT 60
            |-|||| |||| |||| |-|| |||||||
Db   10677 CCGCCGCCGAGGTCCGTCGTCCCGCCCGCCGGGCCTGCCCTGCCGTGGTT 10618

Qy   61 CATCGTCGAGTCGGCGGCCGCCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGC 118
            | ||| ||||| || ||| ||||| | |||| |-|| |||| |||-|| |-||
Db   10617 GACCGGCGCGCCGCCGCCGACCCGCCGATCCGCCGGGTGAGCCCGCTGAGCAGCGGCGCCAGC 10560

RESULT 15
US-10-271-889-48
; Sequence 48, Application US/10271889
; GENERAL INFORMATION:
;   APPLICANT: Sherman, D.H.
;   APPLICANT: Liu, H.
;   APPLICANT: Xue, Y.
;   APPLICANT: Zhao, L.
;   TITLE OF INVENTION: DNA Encoding Methymycin and Pikromycin
;   FILE REFERENCE: 600.582US1
;   CURRENT APPLICATION NUMBER: US/10/271,889
;   CURRENT FILING DATE: 2002-10-15
;   PRIOR APPLICATION NUMBER: US 09/861,289
;   PRIOR FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: US 09/860,846
;   PRIOR FILING DATE: 2001-05-18
;   PRIOR APPLICATION NUMBER: US 09/836,821
;   PRIOR FILING DATE: 2001-04-17
;   PRIOR APPLICATION NUMBER: US 09/105,537

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;   PRIOR FILING DATE: 1998-06-26
;   NUMBER OF SEQ ID NOS: 55
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 48
;     LENGTH: 36778
;     TYPE: DNA
;     ORGANISM: Streptomyces venezuelae
US-10-271-889-48

Query Match      18.4%;   Score 28.4;   DB 6;   Length 36778;
Best Local Similarity   52.5%;   Pred. NO. 23;
Matches    62;  Conservative   0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy     37 GCGGCCGGAGCTGGTCATCTCGCTCATCGTCCGAGTCCGGCCGCCGACTCGACGATGAG 96
          !! ! !!  !!!! !!!  ! !!!!! ! !! ! !!! !! !!!!! !! !! !! !! !!
Db  26247 GCTGGCGCCGCTGCTCACCCGGCTCACCCGGCGATCGCGGTCGGCGCGCCGGTCAA 26306

Qy     97 CGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
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Db  26307 CCAGCCGCAGGGCAGCCGCCGGAGGGCCGGAGGGCGGACACGGACCTCGGCGGGCGG 26364

Search completed: November 19, 2002, 05:29:53
Job time : 194 secs
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          GenCore version 5.1.3
          Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:  November 19, 2002, 05:26:44 ; Search time 2117 Seconds
                                       (without alignments)
                           1178.132 Million cell updates/sec

Title:          US-09-887-194A-13
Perfect score:  154
Sequence:     1 cggccggagctggtcatctc.........gagatgaccagctccggccg 154

Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:  16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters:  32308132

Minimum DB seq length:  0
Maximum DB seq length:  2000000000

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :  EST:*
             1: em_estba:*
             2: em_esthum:*
             3: em_estin:*
             4: em_estmu:*
             5: em_estov:*
             6: em_estpl:*
             7: em_estro:*
             8: em_htc:*
             9: gb_est1:*
            10: gb_est2:*
            11: gb_htc:*
            12: gb_est3:*
            13: gb_est4:*
            14: gb_est5:*
            15: em_estfun:*
            16: em_estom:*
            17: gb_gss:*
            18: em_gss_hum:*
            19: em_gss_inv:*
            20: em_gss_pln:*
            21: em_gss_vrt:*
            22: em_gss_fun:*
            23: em_gss_mam:*
            24: em_gss_mus:*
            25: em_gss_other:*
            26: em_gss_pro:*
            27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	36.6	23.8	175	12	BF945949	BF945949 CMO-NN115
c	2	36.6	23.8	175	12	BF945949	BF945949 CMO-NN115
c	3	36.2	23.5	627	17	CNS030BV	AL253156 Tetraodon
c	4	36.2	23.5	627	17	CNS030BV	AL253156 Tetraodon
	5	36.2	23.5	787	17	AZ933792	AZ933792 BJ__Ba000
c	6	36.2	23.5	787	17	AZ933792	AZ933792 BJ__Ba000

	No.	Score	%	Length	DB	ID	Description
c	7	36.2	23.5	1057	17	CNS03W2P	AL263194 Tetraodon
c	8	36.2	23.5	1057	17	CNS03W2P	AL263194 Tetraodon
	9	36	23.4	972	17	CNS04TDK	AL306353 Tetraodon
c	10	36	23.4	972	17	CNS04TDK	AL306353 Tetraodon
	11	35.8	23.2	367	14	BQ767987	BQ767987 EBro08_SQ
c	12	35.8	23.2	367	14	BQ767987	BQ767987 EBro08_SQ
	13	35.4	23.0	590	9	AI399069	AI399069 NCW01B11T
c	14	35.4	23.0	590	9	AI399069	AI399069 NCW01B11T
c	15	35	22.7	441	12	BF483067	BF483067 WHE2314_D
	16	35	22.7	441	12	BF483067	BF483067 WHE2314_D
	17	35	22.7	571	14	BQ805125	BQ805125 WHE3563_B
c	18	35	22.7	571	14	BQ805125	BQ805125 WHE3563_B
c	19	34.8	22.6	430	12	BG279219	BG279219 b1f04np.r
	20	34.8	22.6	430	12	BG279219	BG279219 b1f04np.r
c	21	34.8	22.6	497	9	AL829848	AL829848 AL829848
	22	34.8	22.6	497	9	AL829848	AL829848 AL829848
	23	34.8	22.6	558	9	AI397686	AI397686 NCC1D1T3
	24	34.8	22.6	558	9	AI397686	AI397686 NCC1D1T3
c	25	34.8	22.6	673	14	BQ841269	BQ841269 WHE4209_A
	26	34.8	22.6	673	14	BQ841269	BQ841269 WHE4209_A
c	27	34.6	22.5	1012	17	CNS03D7T	AL238754 Tetraodon
	28	34.6	22.5	1012	17	CNS03D7T	AL238754 Tetraodon
c	29	34.4	22.3	415	12	BF462402	BF462402 UI-M-CG0p
	30	34.4	22.3	415	12	BF462402	BF462402 UI-M-CG0p
c	31	34.4	22.3	503	12	BF466956	BF466956 UI-M-CG0p
	32	34.4	22.3	503	12	BF466956	BF466956 UI-M-CG0p
c	33	34.4	22.3	769	17	BH555985	BH555985 BOHER70TF
	34	34.4	22.3	769	17	BH555985	BH555985 BOHER70TF
c	35	34.4	22.3	771	17	BH447921	BH447921 BOGHE53TR
	36	34.4	22.3	771	17	BH447921	BH447921 BOGHE53TR
c	37	34.2	22.2	288	14	BQ756129	BQ756129 EBem05_SQ
	38	34.2	22.2	288	14	BQ756129	BQ756129 EBem05_SQ
c	39	34.2	22.2	500	12	BG366731	BG366731 HVSME1000
	40	34.2	22.2	500	12	BG366731	BG366731 HVSME1000
c	41	34.2	22.2	551	14	BQ464534	BQ464534 HF02122r
	42	34.2	22.2	551	14	BQ464534	BQ464534 HF02122r
c	43	34.2	22.2	647	13	BI960178	BI960178 HVSMEn002
	44	34.2	22.2	647	13	BI960178	BI960178 HVSMEn002
c	45	34.2	22.2	669	9	AU078265	AU078265 AU078265

ALIGNMENTS

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RESULT 1
BF945949
LOCUS       BF945949    175 bp    mRNA    linear    EST 22-JAN-2001
DEFINITION  CMO-NN1155-271000-628-a09 NN1155 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF945949
VERSION     BF945949.1  GI:12363224
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 175)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Matsukuma,A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory for Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
```

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM06t2=CM0-NN1155-
271000-628-a09t3-2000-10-27t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13

FEATURES   Location/Qualifiers
     source   1..175
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NN1155"
                     /dev_stage="Adult"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."

BASE COUNT   41 a   38 c   69 g   27 t
ORIGIN

Query Match   23.8%;   Score 36.6; DB 12; Length 175;
Best Local Similarity   65.1%;   Pred. No. 36;
Matches   54;   Conservative   0;   Mismatches   29;   Indels   0;   Gaps   0;

Qy   70 GTCGGGCGGCCCCGACTCCGACGATGAGCCAGATGACCAGCTCCGGCCGCCGCCGACTCCGACGA 129
          ||| || | |||| | || |||||| | ||||| ||| ||| || || |||| || ||||
Db   7 GTCTGTGCGGTAGGCTGGGTGGTGAGGGAAAGGACCACCGTCGGGCGGTAGGCTGGGTGG 66

Qy   130 TGAGCCGGATGACCAGCTCCGGC 152
          ||| || ||||||||| || |||
Db   67 TGAGAAATGACCACGTCGGGC 89

RESULT 2
BF945949/c
LOCUS   BF945949   175 bp   mRNA   linear   EST 22-JAN-2001
DEFINITION CM0-NN1155-271000-628-a09 NN1155 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF945949
VERSION   BF945949.1 GI:12363224
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 175)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPSP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM06t2=CM0-NN1155-
            271000-628-a09t3-2000-10-27t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 13

High quality sequence stop: 175.
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NN1155"
                     /dev_stage="Adult"
                     /note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."

BASE COUNT   41 a   38 c   69 g   27 t
ORIGIN

Query Match   23.8%;   Score 36.6; DB 12; Length 175;
Best Local Similarity   65.1%;   Pred. No. 36;
Matches   54;   Conservative   0;   Mismatches   29;   Indels   0;   Gaps   0;

Qy   3 GCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCA 62
          ||| || |||||||| || |||| || ||| || | |||| | ||||| |||| || ||||
Db   89 GCCCGACGTGGTCATTTCTCACCACCACCCGCCTACCGCCCGACGTGGTCCTTTCCCTCA 30

Qy   63 TCCTCGAGTCGGCGGCCGGAC 85
          | |||| ||| |||| | ||||
Db   29 CCACCCAGCTACCGCCCACAGAC 7

RESULT 3
CNS03OBV
LOCUS   CNS03OBV   627 bp   DNA   linear   GSS 17-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
            041B18 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL253156
VERSION   AL253156.1 GI:7974168
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis.
ORGANISM   Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 627)
AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
TITLE   Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 627)
AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
TITLE   Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 627)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
     source   1..627
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="041B18"
                     /clone_lib="G"

BASE COUNT
ORIGIN

Query Match   139 a   168 c   210 g   105 t   5 others
Best Local Similarity   23.5%;   Score 36.2;   DB 17;   Length 627;
Matches   53;   Conservative   0;   Mismatches   28;   Indels   0;   Gaps   0;

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Qy    55 CTCGCTCATCGTCGAGTCGGCGGCCGGCCGACTCGCGACGATGAGCGAGATGACCAGCTCCGG 114
          ||||||||| ||| ||||||| | ||||||| | ||||| | ||||| | |||||
Db   342 CTCGCTCATGGTCTCGTCGGCGGAGACGTCTCGGACAGGCGGCAGAACAGCAGAGGCGG 401

Qy   115 CCGCCGACTCGACGATGAGCG 135
          ||| | ||| | ||  | ||
Db   402 CCGGCTCCGGACCATGGTCCG 422
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RESULT 4
CNS030BV/c
LOCUS   CNS030BV   627 bp   DNA   linear   GSS 17-MAY-2000
DEFINITION   Tetraodon nigroviridis genome survey sequence T7 end of clone
               041B18 of library G from Tetraodon nigroviridis, genomic survey
               sequence.
ACCESSION   AL253156
VERSION   AL253156.1   GI:7974168
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
ORGANISM   Tetraodon nigroviridis
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
               Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
               Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 627)
AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
               Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
               Saurin,W. and Weissenbach,J.
TITLE   Human gene number estimate provided by genome wide analysis using
               Tetraodon nigroviridis DNA sequence
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 627)
AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
               Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
               Weissenbach,J.
TITLE   Charaterization and repeat analysis of the compact genome of the
               freshwater pufferfish Tetraodon nigroviridis
JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 627)
AUTHORS   Genoscope.
TITLE   Direct Submission
JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
               scale clone-end sequencing project of the Tetraodon nigroviridis
               genome. For more information, please take a look at
               http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
source   1..627
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               /db_xref="taxon:99883"
               /clone="041B18"
               /clone_lib="G"
               /note="Genoscope sequence ID : COBG04lDA09LPl-end : T7"
BASE COUNT   139 a   168 c   210 g   105 t   5 others
ORIGIN

Query Match   23.5%;   Score 36.2;   DB 17;   Length 627;
Best Local Similarity   68.5%;   Pred. No. 54;
Matches   50;   Conservative   0;   Mismatches   23;   Indels   0;   Gaps   0;

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Qy    28 GTCGAGTCGGCGGCCGGCCGAGCTCGCGACGATCGTCATCTCCGCTCATCGTCCGAGTCGGCGGCCGGCCGACTC 87
          ||| | ||| | |||||| ||| ||| | ||||||| | |||| |||| | ||| | |||||||
Db   414 GTCCCGGAGCCGGCCGGCCTGCGCCTGTCTGCTGTTCTCCGCGCCTGCGCGATCCTGCCGAGACGTCCTCCGCCGACGA 355

Qy    88 GACGATGAGCGAG 100
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Db   354 GACCATGAGCGAG 342
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RESULT 5
AZ933792
LOCUS   AZ933792   787 bp   DNA   linear   GSS 24-APR-2001
DEFINITION   BJ_Ba0001E22f B. japonicum BAC library Bradyrhizobium japonicum
               genomic, DNA sequence.
ACCESSION   AZ933792
VERSION   AZ933792.1   GI:13775852
KEYWORDS   GSS.
SOURCE   Bradyrhizobium japonicum
ORGANISM   Bradyrhizobium japonicum
               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
               Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE   1 (bases 1 to 787)
AUTHORS   Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., Goicoechea
               ,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
TITLE   A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
               genome
JOURNAL   Genome Res. 11 (8), 1434-1440 (2001)
MEDLINE   21376150
COMMENT   Contact: Wing RA
               Clemson University Genomics Institute
               Clemson University
               100 Jordan Hall, Clemson, SC 29634, USA
               Tel: 864 656 7288
               Fax: 864 656 4293
               Email: rwing@clemson.edu
               Class: BAC ends
               High quality sequence start: 10
               High quality sequence stop: 732.
FEATURES   Location/Qualifiers
source   1..787
               /organism="Bradyrhizobium japonicum"
               /strain="USDA110"
               /db_xref="taxon:375"
               /clone_lib="B. japonicum BAC library"
               /lab_host="E. coli"
               /note="Vector: pindigo536; Site_1: HindIII"
BASE COUNT   111 a   241 c   267 g   167 t   1 others
ORIGIN

Query Match   23.5%;   Score 36.2;   DB 17;   Length 787;
Best Local Similarity   60.8%;   Pred. No. 56;
Matches   59;   Conservative   0;   Mismatches   38;   Indels   0;   Gaps   0;

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Qy    19 TCGCTCATCGTCCGAGTCGGCGGCCGGCCGAGCTGGTCATCTCCTCATCGTCGAGTCGGCGGC 78
          || |||| | ||||| | ||||| ||| ||| || || | ||| |||| |||| ||||||| ||
Db   349 TCCCTTTCCGTCGATGAAGCGTCCGCTGGTCGCGATCCTGCGCGGCCGTCAAGCCGGAGGA 408

Qy    79 CGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGC 115
          |||||| || | ||||||| ||| | |||| |||||
Db   409 GGCCGAGTCCATCGTCCAGCGTGCTGATCGAGGCCCGGC 445
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RESULT 6
AZ933792/c
LOCUS   AZ933792   787 bp   DNA   linear   GSS 24-APR-2001
DEFINITION   BJ_Ba0001E22f B. japonicum BAC library Bradyrhizobium japonicum
               genomic, DNA sequence.
ACCESSION   AZ933792
VERSION   AZ933792.1   GI:13775852
KEYWORDS   GSS.
SOURCE   Bradyrhizobium japonicum
ORGANISM   Bradyrhizobium japonicum
               Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
               Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE   1 (bases 1 to 787)
AUTHORS   Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., Goicoechea
               ,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
TITLE   A marker-dense, sequence-ready map of the Bradyrhizobium japonicum

JOURNAL   genome
             Genome Res. 11 (8), 1434-1440 (2001)
MEDLINE   21376150
COMMENT   Contact: Wing RA
             Clemson University Genomics Institute
             Clemson University
             100 Jordan Hall, Clemson, SC 29634, USA
             Tel: 864 656 7288
             Fax: 864 656 4293
             Email: rwing@clemson.edu
             Class: BAC ends
             High quality sequence start: 10
             High quality sequence stop: 732.
FEATURES   Location/Qualifiers
     source 1..787
             /organism="Bradyrhizobium japonicum"
             /strain="USDAll0"
             /db_xref="taxon:375"
             /clone_lib="B. japonicum BAC library"
             /lab_host="E. coli"
             /note="Vector: pIndigo536; Site_1: HindIII"
             1 others

BASE COUNT   111 a   241 c   267 g   167 t   1 others
ORIGIN

Query Match   23.5%;   Score 36.2;   DB 17;   Length 787;
Best Local Similarity 60.8%;   Pred. No. 56;
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Qy   40 GCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGGCCGCCGACTCGACGATGAGCGA 99
         ||||| | |||| ||||| ||| |||||| || |||| | |||||||||| |||
Db  445 GCCGGCCTCGATCAGCACGCGTGACGATGGACTCGGCCTCCTCCGGCGTTGACCGCCGCAG 386

Qy  100 GATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGA 136
         ||| | ||| ||| | ||||||||| ||||||
Db  385 GATCGGCGACCAGCGACGCGTTCATCGACGCGAAAGGGA 349
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RESULT 7
CNS03W2P
LOCUS   CNS03W2P   1057 bp   DNA   linear   GSS 18-MAY-2000
DEFINITION   Tetraodon nigroviridis genome survey sequence T7 end of clone
             063I18 of library G from Tetraodon nigroviridis, genomic survey
             sequence.
ACCESSION   AL263194
VERSION   AL263194.1 GI:7984845
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM   Tetraodon nigroviridis
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
             Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
             Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 1057)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
             Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
             Saurin,W. and Weissenbach,J.
  TITLE   Human gene number estimate provided by genome wide analysis using
             Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1057)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
             Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
             Weissenbach,J.
  TITLE   Charaterization and repeat analysis of the compact genome of the
             freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 1057)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
             scale clone-end sequencing project of the Tetraodon nigroviridis
             genome. For more information, please take a look at
             http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
     source 1..1057
             /organism="Tetraodon nigroviridis"
             /db_xref="taxon:99883"
             /clone="063I18"
             /clone_lib="G"
             /note="Genoscope sequence ID : COBG063BE09LP1-end : T7"
             4 others

BASE COUNT   226 a   296 c   323 g   208 t   4 others
ORIGIN

Query Match   23.5%;   Score 36.2;   DB 17;   Length 1057;
Best Local Similarity 65.4%;   Pred. No. 58;
Matches 53; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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Qy   55 CTCGCTCATCGTCGAGTCGGCGGGCCGCCCGACTCGACGATGAGCGAGATGACCAGCTCCGG 114
         |||||||| ||| ||||||| | ||||||| | ||||| | |||||| ||| |||
Db  498 CTCGCTCATGGTCTCGTCGGGAGACGCTCTCGGACAGCGCCGGAGAACAGCAGCAGGCGG 557

Qy  115 CCGCCGACTCGACGATGAGCG 135
         ||| | |||
Db  558 CCGGCTCCCGACACATGGTCCG 578
```

RESULT 8
CNS03W2P/c
LOCUS   CNS03W2P   1057 bp   DNA   linear   GSS 18-MAY-2000
DEFINITION   Tetraodon nigroviridis genome survey sequence T7 end of clone
             063I18 of library G from Tetraodon nigroviridis, genomic survey
             sequence.
ACCESSION   AL263194
VERSION   AL263194.1 GI:7984845
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM   Tetraodon nigroviridis
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
             Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
             Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 1057)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
             Bernot.A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
             Saurin,W. and Weissenbach,J.
  TITLE   Human gene number estimate provided by genome wide analysis using
             Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1057)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
             Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
             Weissenbach,J.
  TITLE   Charaterization and repeat analysis of the compact genome of the
             freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 1057)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
             scale clone-end sequencing project of the Tetraodon nigroviridis
             genome. For more information, please take a look at
             http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
     source 1..1057
             /organism="Tetraodon nigroviridis"
             /db_xref="taxon:99883"
             /clone="063I18"
             /clone_lib="G"
             /note="Genoscope sequence ID : COBG063BE09LP1-end : T7"
             4 others

BASE COUNT   226 a   296 c   323 g   208 t   4 others
ORIGIN

Query Match   23.5%;   Score 36.2;   DB 17;   Length 1057;
Best Local Similarity 68.5%;   Pred. NO. 58;

Right column

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Matches    50;   Conservative   0;   Mismatches   23;   Indels   0;   Gaps   0;

Qy    28  GTCGAGTCGGCGGCGGAGCTGGTCATCGTCGCTCATCGTCGAGCGTCGGCGGCCGCCGACTC  87
          ||| |-| |||||| ||| |-| ||||||| ||||  |||||| || |-|| ||||||||
Db   570  GTCCGGGAGCCGGCCGCCGCCTGTCTGTTCGCGCCCTGTCCGAGACGTCCTCCGCCGACGA  511

Qy    88  GACGATGAGCGAG  100
          ||| |||||||||
Db   510  GACCATGAGCGAG  498
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RESULT 9
CNS04TDK

LOCUS   CNS04TDK   972 bp   DNA   linear   GSS 24-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T3 end of clone
            013I12 of library A from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL306353
VERSION   AL306353.1 GI:8204690
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 972)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE   Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 972)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE   Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 972)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
     source   1..972
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="013I12"
                     /clone_lib="A"
                     /note="Genoscope sequence ID : C1AA003ZE01A1-end : T3"
BASE COUNT   233 a   254 c   267 g   152 t   66 others
ORIGIN

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Query Match             23.4%;  Score 36;  DB 17;  Length 972;
Best Local Similarity   60.0%;  Pred. No. 64;
Matches   57;  Conservative   0;  Mismatches   38;  Indels   0;  Gaps   0;

Qy     6  GGAGCTGGTCATCGTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCG   65
          || || |- || ||| ||| ||||| | ||| ||||| || ||| ||| | ||| |-|
Db   568  GGTTCTCCTNGGGTCGGACGATGTCCGGGAACCGGCGGCCCTNTGCGTTGTTCTCNGCCGCCTGT  509

Qy    66  TCGAGTCGGCGGCGGCCGACTCGACGATGAGCGAG  100
          | || ||| ||| |-| ||||| | |||||||||
Db   508  CCGGAGACGTCCTCCGCCGACGAGACCATGAGCGAG  474
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RESULT 11
BQ767987
LOCUS   BQ767987   367 bp   mRNA   linear   EST 26-JUL-2002
DEFINITION EBro08_SQ010_K07_R root, 3 week, drought-stressed, cv Optic, EBro08
            Hordeum vulgare cDNA clone EBro08_SQ010_K07 5', mRNA sequence.
ACCESSION   BQ767987
VERSION   BQ767987.1 GI:21976461
KEYWORDS   EST.
SOURCE   Hordeum vulgare
  ORGANISM Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 367)
  AUTHORS   Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,

Left column

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Matches    50;   Conservative   0;   Mismatches   23;   Indels   0;   Gaps   0;

Qy    28  GTCGAGTCGGCGGCGGAGCTGGTCATCGTCGCTCATCGTCGAGCGTCGGCGGCCGCCGACTC  87
          ||| |-| |||||| ||| |-| ||||||| ||||  |||||| || |-|| ||||||||
Db   570  GTCCGGGAGCCGGCCGCCGCCTGTCTGTTCGCGCCCTGTCCGAGACGTCCTCCGCCGACGA  511

Qy    88  GACGATGAGCGAG  100
          ||| |||||||||
Db   510  GACCATGAGCGAG  498
```

RESULT 9
CNS04TDK

LOCUS   CNS04TDK   972 bp   DNA   linear   GSS 24-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T3 end of clone
            013I12 of library A from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL306353
VERSION   AL306353.1 GI:8204690
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 972)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE   Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 972)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE   Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 972)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT   This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
     source   1..972
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="013I12"
                     /clone_lib="A"
                     /note="Genoscope sequence ID : C1AA003ZE01A1-end : T3"
BASE COUNT   233 a   254 c   267 g   152 t   66 others
ORIGIN

```
Query Match             23.4%;  Score 36;  DB 17;  Length 972;
Best Local Similarity   60.0%;  Pred. No. 64;
Matches   57;  Conservative   0;  Mismatches   38;  Indels   0;  Gaps   0;

Qy    55  CTCGGCTCATCGTCGAGTCGGCGGCGGCCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGG  114
          |||||||| |-| ||||||||| | ||| |- ||| | || |-||| || |||
Db   474  CTCGCTCATCGGTCTCGGCGGGAGGACGTCTCGGACAGCCGCAGGAACACAGCANAGGCGG  533

Qy   115  CCGCCGACTCGACGATGAGCGAGATGACCAGCTCC  149
          ||-| |-| || |-| ||||| | |-|| |
Db   534  CCGGCTCCCGGACATCCTCCGACCCNAGGAGAACC  568
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RESULT 10
CNS04TDK/c

TITLE   Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
            Development of Barley Transcriptome Resources
JOURNAL   Unpublished (2001)
COMMENT   Contact: Waugh R, Marshall DF
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scri.sari.ac.uk.
FEATURES   Location/Qualifiers
     source 1..367
            /organism="Hordeum vulgare"
            /cultivar="Optic"
            /db_xref="taxon:4513"
            /clone="EBro08_SQ010_K07"
            /clone_lib="root, 3 week, drought-stressed, cv Optic,
            EBro08"
            /tissue_type="root"
            /dev_stage="3 week"
            /lab_host="DH10B"
            /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
            Non-normalised library, directionally cloned into pSPORT1.
            Derived from roots of 3 week old drought stressed barley
            plants. Developed as part of the barley transcriptome
            resources of BBSRC/SEERAD funded cereal IGF (Investigating
            Gene Function) project."
BASE COUNT   61 a   153 c   116 g   37 t
ORIGIN

Query Match   23.2%;   Score 35.8; DB 14; Length 367;
Best Local Similarity 55.1%;   Pred. No. 62;
Matches   70; Conservative   0; Mismatches   57; Indels   0; Gaps   0;

Qy   1 CGGCCGGAGCTGGTCATCTCGTCAGTCGTCGAGTCCGGCCGAGCTGGTCATCTCGT   60
          ||||||||||| |||| | ||||||||| ||| ||| ||||||||||||||||||
Db   220 CGGCAGCAGCGGCGACGAGCACCGGGAGCCACGGTGCCCCGACCTCAACCTCGACCT 279

Qy   61 CATCGTCGAGTCGCGGCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCG 120
          |||| ||| |||||| |||||| | ||||||| | || ||||||||||||
Db   280 GTCCGGTGGCCCCGCCCGGCGGCCGACACGCCGACGTCGCTCGCCTCGCCCTGCCGCCA 339

Qy   121 ACTCGAC 127
          |||| |
Db   340 CCTCGGC 346

RESULT 12
BQ767987/c
LOCUS   BQ767987   367 bp   mRNA   linear   EST 26-JUL-2002
DEFINITION EBro08_SQ010_K07_R root, 3 week, drought-stressed, cv Optic, EBro08
            Hordeum vulgare cDNA clone EBro08_SQ010_K07 5', mRNA sequence.
ACCESSION   BQ767987
VERSION   BQ767987.1 GI:21976461
KEYWORDS   EST.
SOURCE   Hordeum vulgare
  ORGANISM Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 367)
  AUTHORS   Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
            Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
  TITLE   Development of Barley Transcriptome Resources
  JOURNAL   Unpublished (2001)
COMMENT   Contact: Waugh R, Marshall DF
            Genome Dynamics/Computational Biology
            Scottish Crop Research Institute
            Invergowrie, Dundee, DD2 5DA, Scotland, UK
            Tel: 00 44 1382 562731
            Fax: 00 44 1382 562426
            Email: est@scri.sari.ac.uk.
FEATURES   Location/Qualifiers

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     source
            /organism="Hordeum vulgare"
            /cultivar="Optic"
            /db_xref="taxon:4513"
            /clone="EBro08_SQ010_K07"
            /clone_lib="root, 3 week, drought-stressed, cv Optic,
            EBro08"
            /tissue_type="root"
            /dev_stage="3 week"
            /lab_host="DH10B"
            /note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
            Non-normalised library, directionally cloned into pSPORT1.
            Derived from roots of 3 week old drought stressed barley
            plants. Developed as part of the barley transcriptome
            resources of BBSRC/SEERAD funded cereal IGF (Investigating
            Gene Function) project."
BASE COUNT   61 a   153 c   116 g   37 t
ORIGIN

Query Match   23.2%;   Score 35.8; DB 14; Length 367;
Best Local Similarity 55.1%;   Pred. No. 62;
Matches   70; Conservative   0; Mismatches   57; Indels   0; Gaps   0;

Qy   28 GTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGCCGACTC   87
          ||||| |||||| || |||||| ||| | | ||||| |||||| || |||| ||
Db   346 GCCCAGGTGGCGGCCAGAGGCAGACCGGGTGCGACGTCGGCGTGTCGGCCGCGGCGGGCC 287

Qy   88 GACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCT 147
          ||| || ||| || || ||||||| || ||| ||||| || ||| | |||| ||
Db   286 CACGGACAGGTCGAGGTTGAGGTCGGGGCACCGGTGCCCCGGTCCCCGGTGCTCGTCGTCG 227

Qy   148 CCGCCG 154
          | ||||
Db   226 GCTCCG 220

RESULT 13
AI399069
LOCUS   AI399069.   590 bp   mRNA   linear   EST 08-FEB-1999
DEFINITION NCW01B11T3 Westergaards Neurospora crassa cDNA clone W01B11 5',
            mRNA sequence.
ACCESSION   AI399069
VERSION   AI399069.1 GI:4242154
KEYWORDS   EST.
SOURCE   Neurospora crassa
  ORGANISM Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora.
REFERENCE   1 (bases 1 to 590)
  AUTHORS   Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
            Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
            Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R.
            , Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R.,
            Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig
            ,D.O.
  TITLE   Expressed sequences from conidial, mycelial, and sexual stages of
            Neurospora crassa
  JOURNAL   Fungal Genet. Biol. 21, 348-363 (1997)
  MEDLINE   97435549
COMMENT   Contact: Natvig,D.O./Nelson,M.A.
            Department of Biology
            University of New Mexico
            Castetter Hall, Albuquerque, NM 87131, USA
            Tel: 505 277 3411
            Fax: 505 277 0304
            Email: ngp@biology.unm.edu.
FEATURES   Location/Qualifiers
     source 1..590
            /organism="Neurospora crassa"
            /strain="74-OR23-IV A (FGSC 2489)"
            /db_xref="taxon:5141"
            /clone="W01B11"
            /clone_lib="Westergaards"

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                /sex="Mating type A"
                /tissue_type="Unfertilized sexual tissue"
                /dev_stage="Unfertilized sexual stage"
                /lab_host="E. coli"
                /note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2:
                XhoI; Westergaard's medium (Nitrogen limiting). Floating
                mycelial mats grown at 25C for 36 hours. cDNA
                directionally cloned into pBluescript SK(-) using the
                Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
BASE COUNT    94 a    226 c    138 g    131 t
ORIGIN

Query Match
Best Local Similarity   23.0%;         Score 35.4; DB 9; Length 590;
                        57.3%;         Pred. No. 82;
Matches   63; Conservative  0; Mismatches 47; Indels  0; Gaps  0;

Qy  18 CTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGG 77
       |||||||||| |  |||||  |||| ||| | | |||||| || | ||| |||||  |||
Db  81 CTCGCTCATCGCCCCAGAAGCCCCGCGCCAACAGCCTCCTCGCTCGCGCCGCCGACTGCGCCCG 140

Qy  78 CCGCGCGACTCGACGATGAGCGAGATGACCAGCTCCGGCGCCGACTCGAC 127
       ||||  | |  ||  ||  ||| |||| |||| |||| ||| ||
Db 141 CCGCGGTTACCANTACCAGTCTCATACTCAGCCCCAGCCGGACAGTGCCC 190

RESULT 14
AI399069/c
LOCUS       AI399069               590 bp    mRNA       linear   EST 08-FEB-1999
DEFINITION  NCW01B11T3 Westergaards Neurospora crassa cDNA clone W01B11 5',
            mRNA sequence.
ACCESSION   AI399069
VERSION     AI399069.1  GI:4242154
KEYWORDS    EST.
SOURCE      Neurospora crassa.
ORGANISM    Neurospora crassa
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Sordariales; Sordariaceae; Neurospora
REFERENCE   1 (bases 1 to 590)
AUTHORS     Nelson,M.A., Kang,S., Braun,E.L., Crawford,M.E., Dolan,P.L.,
            Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
            Cushing,T., Errett,A., Fleharty,M., Gorman,M., Judson,K., Miller,R.
            , Ortega,J., Pavlova,I., Perea,J., Todisco,S., Trujillo,R.,
            Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S. and Natvig
            ,D.O.
TITLE       Expressed sequences from conidial, mycelial, and sexual stages of
            Neurospora crassa
JOURNAL     Fungal Genet. Biol. 21, 348-363 (1997)
MEDLINE     97435549
COMMENT     Contact: Natvig,D.O./Nelson,M.A.
            Department of Biology
            University of New Mexico
            Castetter Hall, Albuquerque, NM 87131, USA
            Tel: 505 277 3411
            Fax: 505 277 0304
            Email: ngp@biology.unm.edu.
FEATURES             Location/Qualifiers
     source          1..590
                     /organism="Neurospora crassa"
                     /strain="74-OR23-IV A (FGSC 2489)"
                     /db_xref="taxon:5141"
                     /clone="W01B11"
                     /clone_lib="Westergaards"
                     /sex="Mating type A"
                     /tissue_type="Unfertilized sexual tissue"
                     /dev_stage="Unfertilized sexual stage"
                     /lab_host="E. coli"
                     /note="Vector: pBluescript SK (-); Site_1: EcoRI; Site_2:
                     XhoI; Westergaard's medium (Nitrogen limiting). Floating
                     mycelial mats grown at 25C for 36 hours. cDNA
                     directionally cloned into pBluescript SK(-) using the
                     Uni-ZAP XR vector system (Stratagene, La Jolla, CA)."
BASE COUNT    94 a    226 c    138 g    131 t
ORIGIN
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Query Match
Best Local Similarity   23.0%;         Score 35.4; DB 9; Length 590;
                        57.3%;         Pred. No. 82;
Matches   63; Conservative  0; Mismatches 47; Indels  0; Gaps  0;

Qy  28 GTCGAGTCGGCGGCCGGAGCTGGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGACTC 87
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Db 190 GGCCACTGTCCGGCTGGGGTGAGTATGAGACTGG?ANTGGTAACCGGCGGCGGGCCCCT 131

Qy  88 GACGATGAGCGAGATGACCAGCTCCGGCGCCGACTCCGACGATGAGCGAG 137
       | ||| | ||||||  ||       |||| | | | |  ||||||||||||
Db 130 GGAGACGAGCGAGGAGGCTGTTGGCGGCGGCTTCTGGCCGATGAGCGAG 81

RESULT 15
BF483067
LOCUS       BF483067               441 bp    mRNA       linear   EST 06-DEC-2000
DEFINITION  WHE2314_D05_G10ZS wheat pre-anthesis spike cDNA library Triticum
            aestivum cDNA clone WHE2314_D05_G10, mRNA sequence.
ACCESSION   BF483067
VERSION     BF483067.1  GI:11566368
KEYWORDS    EST.
SOURCE      bread wheat.
ORGANISM    Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 441)
AUTHORS     Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
TITLE       The structure and function of the expressed portion of the wheat
            genomes - Pre-anthesis spike cDNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES             Location/Qualifiers
     source          1..441
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE2314_D05_G10"
                     /clone_lib="wheat pre-anthesis spike cDNA library"
                     /tissue_type="Spike before anthesis"
                     /dev_stage="Adult plant"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
                     greenhouse. Whole spike with awns trimmed, white, green
                     and yellow anther were collected and total RNA, and
                     poly(A) RNA were prepared, a cDNA library was made, and
                     the cDNA clones were in vivo excised to give pBluescript
                     phagemids in the TJ Close lab (Choi, Close, Fenton) at
                     the University of California, Riverside. Plasmid DNA
                     preparations and DNA sequencing were performed in the OD
                     Anderson lab (all other authors)."
BASE COUNT    54 a    168 c    144 g    75 t
ORIGIN

Query Match
Best Local Similarity   22.7%;         Score 35; DB 12; Length 441;
                        63.9%;         Pred. No. 97;
Matches   53; Conservative  0; Mismatches 30; Indels  0; Gaps  0;

Qy  27 CGTCGAGTCGGCGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGACT 86
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Db   20 CGTCGAGGCGGGCGCCGGGCGTCCTCCTCCTCCTCGCGGCGCGTCCGCGGCTT 79

Qy   87 CGACGATGAGCGAGAGATGACCAGC 109
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Db   80 CGGCCAGGGGCGACGGCAACGGGC 102

Search completed: November 19, 2002, 07:49:42
Job time : 2131 secs

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OM nucleic - nucleic search, using sw model

                 GenCore version 5.1.3
                 Copyright (c) 1993 - 2002 Compugen Ltd.

Run on:          November 19, 2002, 05:24:44 ; Search time 2709 Seconds
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                                             1654.423 Million cell updates/sec

Title:           US-09-887-194A-13
Perfect score:   154
Sequence:        1 cggccggagctggtcatctc........gagatgaccagctccggccg 154

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:      4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
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     35:  em_htg_rod:*
     36:  em_htg_mam:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Match Length	DB	ID	Description
1		154	100.0	154	6	AX367128	AX367128 Sequence
2	c	154	100.0	154	6	AX367128	AX367128 Sequence
3		154	100.0	154	6	AX392336	AX392336 Sequence
4	c	154	100.0	154	6	AX392336	AX392336 Sequence
5		112	72.7	4974	6	AX353724	AX353724 Sequence
6	c	112	72.7	4974	6	AX353724	AX353724 Sequence
7		82.8	53.8	6611	6	AX392337	AX392337 Sequence
8	c	82.8	53.8	6611	6	AX392337	AX392337 Sequence
9		81	52.6	963	6	AX367144	AX367144 Sequence
10	c	81	52.6	963	6	AX367144	AX367144 Sequence
11		80	51.9	80	6	AX367127	AX367127 Sequence
12	c	80	51.9	80	6	AX367127	AX367127 Sequence
13		80	51.9	80	6	AX392335	AX392335 Sequence
14	c	80	51.9	80	6	AX392335	AX392335 Sequence
15		80	51.9	92	6	AX367129	AX367129 Sequence
16	c	80	51.9	92	6	AX367129	AX367129 Sequence
17		45.8	29.7	1717	6	AX367139	AX367139 Sequence
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19		38.2	24.8	10348	1	AE004846	AE004846 Pseudomon
20	c	38.2	24.8	10348	1	AE004846	AE004846 Pseudomon
21		36.4	23.6	115036	2	AC107207	AC107207 Oryza sat
22	c	36.4	23.6	115036	2	AC107207	AC107207 Oryza sat
23		36.2	23.5	8973	1	AY081837	AY081837 Bradyrhiz
24	c	36.2	23.5	8973	1	AY081837	AY081837 Bradyrhiz
25		36.2	23.5	123169	9	AC008771	AC008771 Homo sapi
26	c	36.2	23.5	123169	9	AC008771	AC008771 Homo sapi
27		36.2	23.5	126054	9	AC018764	AC018764 Homo sapi
28	c	36.2	23.5	126054	9	AC018764	AC018764 Homo sapi
29		36	23.4	131603	2	AC097280	AC097280 Oryza sat
30	c	36	23.4	131603	2	AC097280	AC097280 Oryza sat
31		36	23.4	190050	1	AL646059	AL646059 Ralstonia
32	c	36	23.4	190050	1	AL646059	AL646059 Ralstonia
33		35.8	23.2	1102	8	HVMYB2	X70876 H.vulgare m
34	c	35.8	23.2	1102	8	HVMYB2	X70876 H.vulgare m
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36	c	35.8	23.2	22115	1	SCC22	AL096839 Streptomy
37		35.8	23.2	106161	2	AC120984	AC120984 Oryza sat
38	c	35.8	23.2	106161	2	AC120984	AC120984 Oryza sat
39		35.8	23.2	180186	8	AP003104	AP003104 Oryza sat
40	c	35.8	23.2	180186	8	AP003104	AP003104 Oryza sat
41		35.6	23.1	102529	2	AP004747	AP004747 Oryza sat
42	c	35.6	23.1	102529	2	AP004747	AP004747 Oryza sat
43		35.6	23.1	340900	1	SME591791	AL591791 Sinorhizo
44	c	35.6	23.1	340900	1	SME591791	AL591791 Sinorhizo
45	c	35	22.7	1020	9	AB078417	AB078417 Homo sapi

ALIGNMENTS

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RESULT 1
AX367128
LOCUS        AX367128                    154 bp    DNA       linear   PAT 16-FEB-2002
DEFINITION   Sequence 13 from Patent WO0200904.
ACCESSION    AX367128
VERSION      AX367128.1  GI:18855329
KEYWORDS     .
SOURCE       synthetic construct.
  ORGANISM   synthetic construct
             artificial sequences
REFERENCE    1
  AUTHORS    Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
             and Nichols,S.E.
  TITLE      Recombinant constructs and their use in reducing gene expression
  JOURNAL    Patent: WO 0200904-A 13 03-JAN-2002;
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Pred. No. is the number of results predicted by chance to have a

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FEATURES        source          E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
                                INTERNATIONAL, INC. (US)
                                Location/Qualifiers
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                                /organism="synthetic construct"
                                /db_xref="taxon:32630"
                                /note="ELVISLIVES complementary region of pKS133"
BASE COUNT          24 a       53 c       53 g       24 t
ORIGIN
Query Match        100.0%;   Score 154;  DB 6;  Length 154;
Best Local Similarity  100.0%;  Pred. No. 4.2e-20;
Matches  154;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60
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Db    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60

Qy   61 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120

Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154
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Db  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154


RESULT 2
AX367128/c
LOCUS       AX367128        154 bp    DNA        linear   PAT 16-FEB-2002
DEFINITION  Sequence 13 from Patent WO0200904.
ACCESSION   AX367128
VERSION     AX367128.1  GI:18855329
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
            and Nichols,S.E.
TITLE       Recombinant constructs and their use in reducing gene expression
JOURNAL     Patent: WO 0200904-A 13 03-JAN-2002;
            E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
            INTERNATIONAL, INC. (US)
FEATURES    source
                                Location/Qualifiers
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                                /organism="synthetic construct"
                                /db_xref="taxon:32630"
                                /note="ELVISLIVES complementary region of pKS133"
BASE COUNT          24 a       53 c       53 g       24 t
ORIGIN
Query Match        100.0%;   Score 154;  DB 6;  Length 154;
Best Local Similarity  100.0%;  Pred. No. 4.2e-20;
Matches  154;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  154 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  95

Qy   61 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
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Db   94 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG  35

Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154
          ||||||||||||||||||||||||||||||||||
Db   34 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  1


RESULT 3
AX392336
LOCUS       AX392336        154 bp    DNA        linear   PAT 23-MAR-2002
DEFINITION  Sequence 25 from Patent WO0216565.
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ACCESSION   AX392336
VERSION     AX392336.1  GI:19700689
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE       Nucleotide sequences of a new class of diverged delta-9
            stearoyl-acp desaturase genes
JOURNAL     Patent: WO 0216565-A 25 28-FEB-2002;
            E. I. du Pont de Nemours and Company (US)
FEATURES    source          Location/Qualifiers
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                                /organism="synthetic construct"
                                /db_xref="taxon:32630"
                                /note="ELVISLIVES complementary region of pKS133"
BASE COUNT          24 a       53 c       53 g       24 t
ORIGIN
Query Match        100.0%;   Score 154;  DB 6;  Length 154;
Best Local Similarity  100.0%;  Pred. No. 4.2e-20;
Matches  154;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60
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Db    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60

Qy   61 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120

Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154
          ||||||||||||||||||||||||||||||||||
Db  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG  154


RESULT 4
AX392336/c
LOCUS       AX392336        154 bp    DNA        linear   PAT 23-MAR-2002
DEFINITION  Sequence 25 from Patent WO0216565.
ACCESSION   AX392336
VERSION     AX392336.1  GI:19700689
KEYWORDS
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE       Nucleotide sequences of a new class of diverged delta-9
            stearoyl-acp desaturase genes
JOURNAL     Patent: WO 0216565-A 25 28-FEB-2002;
            E. I. du Pont de Nemours and Company (US)
FEATURES    source          Location/Qualifiers
                                1..154
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                                /db_xref="taxon:32630"
                                /note="ELVISLIVES complementary region of pKS133"
BASE COUNT          24 a       53 c       53 g       24 t
ORIGIN
Query Match        100.0%;   Score 154;  DB 6;  Length 154;
Best Local Similarity  100.0%;  Pred. No. 4.2e-20;
Matches  154;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  154 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCGGCCGGAGCTGGTCATCTCGCT  95

Qy   61 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   94 CATCGTCGAGTCGGCGGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCG  35
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Qy  121 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 154
        ||||||||||||||||||||||||||||||||||
Db   34 ACTCGACGATGAGCGAGATGACCAGCTCCGGCCG 1
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RESULT 5
AX353724
LOCUS   AX353724   4974 bp   DNA   linear   PAT 06-FEB-2002
DEFINITION Sequence 17 from Patent EP1174510.
ACCESSION   AX353724
VERSION   AX353724.1 GI:18618779
KEYWORDS   .
SOURCE   synthetic construct.
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Allen,S.M., Butler,K.H., Carlson,T.J. and Ilag,L.L.
  TITLE   Plastidial phosphoglucomutase genes
  JOURNAL   Patent: EP 1174510-A 17 23-JAN-2002;
            E.I. du Pont de Nemours and Company (US)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32630"
BASE COUNT 1444 a   1070 c   1003 g   1456 t
ORIGIN   1 others

Query Match   72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4863 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGGCGCCGCCGAGCTCGGTCATCTCGCT 4922

Qy   61 CATCGTCGAGTCGCCGGCGCCGCCAGCTCC 112
        ||||||||||||||||||||||||||||||
Db 4923 CATCGTCGAGTCGCCGGCGCCGCCAGCTCC 4974
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RESULT 6
AX353724/c
LOCUS   AX353724   4974 bp   DNA   linear   PAT 06-FEB-2002
DEFINITION Sequence 17 from Patent EP1174510.
ACCESSION   AX353724
VERSION   AX353724.1 GI:18618779
KEYWORDS   .
SOURCE   synthetic construct.
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Allen,S.M., Butler,K.H., Carlson,T.J. and Ilag,L.L.
  TITLE   Plastidial phosphoglucomutase genes
  JOURNAL   Patent: EP 1174510-A 17 23-JAN-2002;
            E.I. du Pont de Nemours and Company (US)
FEATURES   Location/Qualifiers
  source   1..4974
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            /db_xref="taxon:32630"
BASE COUNT 1444 a   1070 c   1003 g   1456 t
ORIGIN   1 others

Query Match   72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 2.4e-12;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   43 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGGCGCCGCCGACTCGCCGGCGATGAGCGAGAT 102
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Db 4974 GGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGGCGCCGCCGACTCGCCGGCGATGAGCGAGAT 4915

Qy  103 GACCAGCTCCGGCGCCGCCGGCGCCGCCGACTCGCCGGCGATGAGCGAGATGACCAGCTCCGGCCG 154
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4914 GACCAGCTCCGGCGCCGCCGGCGCCGCCGACTCGCCGGCGATGAGCGAGATGACCAGCTCCGGCCG 4863
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RESULT 7
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LOCUS   AX392337   6611 bp   DNA   linear   PAT 23-MAR-2002
DEFINITION Sequence 26 from Patent WO0216565.
ACCESSION   AX392337
VERSION   AX392337.1 GI:19700690
KEYWORDS   .
SOURCE   unidentified.
ORGANISM   unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
  TITLE   Nucleotide sequences of a new class of diverged delta-9
            stearoyl-acp desaturase genes
  JOURNAL   Patent: WO 0216565-A 26 28-FEB-2002;
            E.I. du Pont de Nemours and Company (US)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32644"
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ORIGIN   1 others

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Best Local Similarity 97.7%; Pred. No. 8.3e-07;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGGCGCCGCCGAGCTCGTCGTCATCTCGCT 60
        |||||||||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||||
Db 5348 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGCCGGCGCCGCCGGAGCTCGGTCGTCATCTCGCT 5407

Qy   61 CATCGTCGAGTCGCCGGCGCCGCCACT 86
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Db 5408 CATCGTCGAGTCGCCGGCGCCGCTGAGT 5433
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RESULT 8
AX392337/c
LOCUS   AX392337   6611 bp   DNA   linear   PAT 23-MAR-2002
DEFINITION Sequence 26 from Patent WO0216565.
ACCESSION   AX392337
VERSION   AX392337.1 GI:19700690
KEYWORDS   .
SOURCE   unidentified.
ORGANISM   unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
  TITLE   Nucleotide sequences of a new class of diverged delta-9
            stearoyl-acp desaturase genes
  JOURNAL   Patent: WO 0216565-A 26 28-FEB-2002;
            E.I. du Pont de Nemours and Company (US)
FEATURES   Location/Qualifiers
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            /db_xref="taxon:32644"
            /note="plasmid pBS68"
BASE COUNT 1831 a   1472 c   1453 g   1854 t
ORIGIN   1 others

Query Match   53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity 97.7%; Pred. No. 8.3e-07;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy   69 AGTCGCCGGCGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 128
        ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db 5433 ACTCAGCGGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGACTCGACG 5374

Qy  129 ATGAGCGAGATGACCAGCTCCGCCG 154
        |||||||||||||||||||||||||
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Db   5373 ATGAGCGAGATGACCAGCTCCGGCCG 5348

RESULT 9
AX367144
LOCUS   AX367144   963 bp   DNA   linear   PAT 16-FEB-2002
DEFINITION   Sequence 29 from Patent WO0200904.
ACCESSION   AX367144
VERSION   AX367144.1 GI:18855345
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM   synthetic construct
             artificial sequences.
REFERENCE   1
  AUTHORS   Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
             and Nichols,S.E.
  TITLE   Recombinant constructs and their use in reducing gene expression
  JOURNAL   Patent: WO 0200904-A 29 03-JAN-2002;
             E.I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
             INTERNATIONAL, INC. (US)
FEATURES   Location/Qualifiers
     source   1..963
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ELVISLIVES complementary region of pKS149"
BASE COUNT   240 a   243 c   248 g   232 t
ORIGIN

Query Match   52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   74 GCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGCCGACTCGACGATGAG 133
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   883 GCGGCCGCCGACTCGACGATGAGCGAGATGACCAGCTCCGGCCGCCGCCGACTCGACGATGAG 942

Qy   134 CGAGATGACCAGCTCCGGCCG 154
          |||||||||||||||||||||
Db   943 CGAGATGACCAGCTCCGGCCG 963

RESULT 10
AX367144/c
LOCUS   AX367144   963 bp   DNA   linear   PAT 16-FEB-2002
DEFINITION   Sequence 29 from Patent WO0200904.
ACCESSION   AX367144
VERSION   AX367144.1 GI:18855345
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM   synthetic construct
             artificial sequences.
REFERENCE   1
  AUTHORS   Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
             and Nichols,S.E.
  TITLE   Recombinant constructs and their use in reducing gene expression
  JOURNAL   Patent: WO 0200904-A 29 03-JAN-2002;
             E.I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
             INTERNATIONAL, INC. (US)
FEATURES   Location/Qualifiers
     source   1..963
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ELVISLIVES complementary region of pKS149"
BASE COUNT   240 a   243 c   248 g   232 t
ORIGIN

Query Match   52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCGGCCGGAGCTGGTCATCTCGCT 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   963 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCGGCCGGAGCTGGTCATCTCGCT 904

Qy   61 CATCGTCGAGTCGGCGGCCGC 81
          |||||||||||||||||||||
Db   903 CATCGTCGAGTCGGCGGCCGC 883

RESULT 11
AX367127
LOCUS   AX367127   80 bp   DNA   PAT 16-FEB-2002
DEFINITION   Sequence 12 from Patent WO0200904.
ACCESSION   AX367127
VERSION   AX367127.1 GI:18855328
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM   synthetic construct
             artificial sequences.
REFERENCE   1
  AUTHORS   Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
             and Nichols,S.E.
  TITLE   Recombinant constructs and their use in reducing gene expression
  JOURNAL   Patent: WO 0200904-A 12 03-JAN-2002;
             E.I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
             INTERNATIONAL, INC. (US)
FEATURES   Location/Qualifiers
     source   1..80
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ELVISLIVES complementary region of pKS106 and
                     pKS124"
BASE COUNT   12 a   28 c   28 g   12 t
ORIGIN

Query Match   51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCGGCCGGAGCTCGACGATGAGC 97
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGAGTCGGCCGGCGGCCGGAGCTCGACGATGAGC 60

Qy   98 GAGATGACCAGCTCCGGCCG 117
          ||||||||||||||||||||
Db   61 GAGATGACCAGCTCCGGCCG 80

RESULT 12
AX367127/c
LOCUS   AX367127   80 bp   DNA   PAT 16-FEB-2002
DEFINITION   Sequence 12 from Patent WO0200904.
ACCESSION   AX367127
VERSION   AX367127.1 GI:18855328
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM   synthetic construct
             artificial sequences.
REFERENCE   1
  AUTHORS   Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
             and Nichols,S.E.
  TITLE   Recombinant constructs and their use in reducing gene expression
  JOURNAL   Patent: WO 0200904-A 12 03-JAN-2002;
             E.I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
             INTERNATIONAL, INC. (US)
FEATURES   Location/Qualifiers
     source   1..80
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ELVISLIVES complementary region of pKS106 and
                     pKS124"
BASE COUNT   12 a   28 c   28 g   12 t
ORIGIN

Query Match   51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 6e-06;

Matches   80; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 97
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 21

Qy   98 GAGATGACCAGCTCCGGCCG 117
        ||||||||||||||||||||
Db   20 GAGATGACCAGCTCCGGCCG 1

RESULT 13
AX392335
LOCUS   AX392335   80 bp   DNA   linear   PAT 23-MAR-2002
DEFINITION Sequence 24 from Patent WO0216565.
ACCESSION   AX392335
VERSION   AX392335.1 GI:19700688
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
  TITLE   Nucleotide sequences of a new class of diverged delta-9
            stearoyl-acp desaturase genes
  JOURNAL   Patent: WO 0216565-A 24 28-FEB-2002;
            E. I. du Pont de Nemours and Company (US)
FEATURES   Location/Qualifiers
     source   1..80
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ELVISLIVES complementary region of pKS106 and
                     pKS124"
BASE COUNT   12 a   28 c   28 g   12 t
ORIGIN

Query Match   51.9%; Score 80; DB 6; Length 80;
Best Local Similarity   100.0%; Pred. No. 6e-06;
Matches   80; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 97
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 60

Qy   98 GAGATGACCAGCTCCGGCCG 117
        ||||||||||||||||||||
Db   61 GAGATGACCAGCTCCGGCCG 80

RESULT 14
AX392335/c
LOCUS   AX392335   80 bp   DNA   linear   PAT 23-MAR-2002
DEFINITION Sequence 24 from Patent WO0216565.
ACCESSION   AX392335
VERSION   AX392335.1 GI:19700688
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
  TITLE   Nucleotide sequences of a new class of diverged delta-9
            stearoyl-acp desaturase genes
  JOURNAL   Patent: WO 0216565-A 24 28-FEB-2002;
            E. I. du Pont de Nemours and Company (US)
FEATURES   Location/Qualifiers
     source   1..80
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ELVISLIVES complementary region of pKS106 and
                     pKS124"
BASE COUNT   12 a   28 c   28 g   12 t
ORIGIN

Query Match   51.9%; Score 80; DB 6; Length 80;
Best Local Similarity   100.0%; Pred. No. 6e-06;
Matches   80; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 97
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   80 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 21

Qy   98 GAGATGACCAGCTCCGGCCG 117
        ||||||||||||||||||||
Db   20 GAGATGACCAGCTCCGGCCG 1

RESULT 15
AX367129
LOCUS   AX367129   92 bp   DNA   linear   PAT 16-FEB-2002
DEFINITION Sequence 14 from Patent WO0200904.
ACCESSION   AX367129
VERSION   AX367129.1 GI:18B55330
KEYWORDS   .
SOURCE   synthetic construct.
  ORGANISM synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
            and Nichols,S.E.
  TITLE   Recombinant constructs and their use in reducing gene expression
  JOURNAL   Patent: WO 0200904-A 14 03-JAN-2002;
            E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
            INTERNATIONAL, INC. (US)
FEATURES   Location/Qualifiers
     source   1..92
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="ELVISLIVES PCR primer"
BASE COUNT   16 a   30 c   30 g   16 t
ORIGIN

Query Match   51.9%; Score 80; DB 6; Length 92;
Best Local Similarity   100.0%; Pred. No. 5.9e-06;
Matches   80; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   38 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 97
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7 CGGCCGGAGCTGGTCATCTCGCTCATCGTCGTCGAGTCGCGGCGGCCGACTCGACGATGAGC 66

Qy   98 GAGATGACCAGCTCCGGCCG 117
        ||||||||||||||||||||
Db   67 GAGATGACCAGCTCCGGCCG 86

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